

cytochrome-c oxidase (EC 1.9.3.1) chain I - Bipes biporus mitochondrion (fragment)		Matches	3 ;	Conservative	2 ;	Mismatches	2 ;	Indels	0 ;	Gaps	0 ;
C;Species: mitochrondrion Bipes biporus	Qy	5	FSLEWTS 11								
C;Accession: T13838	Db	5	YSRGWTN 11								
RESULT 6											
		PT0519		T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)							
		C;Species: Mus musculus (house mouse)									
		C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997									
		C;Accession: PT0519									
		R;Peeney, A.J.									
		J. Exp. Med. 174, 115-124, 1991									
		A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions									
		A;Reference number: PR0505 ; MUID:91277601 ; PMID:1711558									
		A;Accession: PR0519									
		A;Status: translation not shown									
		A;Molecule type: mRNA									
		A;Residues: 1-6 <FEE>									
		A;Experimental source: adult thymus, strain BALB/c									
		C;Keywords: T-cell receptor									
Query Match	Qy	6	SEIW 9								
Best Local Similarity	Db	2	SSIW 5								
Matches 5 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;											
Query Match	Qy	6	SEIW 9								
Best Local Similarity	Db	2	SSIW 5								
Matches 3 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;											
RESULT 4											
B34835	Qy	6	SEIW 9								
dnaA protein - Pseudomonas aeruginosa (fragment)	Db	2	SSIW 5								
C;Species: Pseudomonas aeruginosa											
C;Accession: B34835											
C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999											
Query Match	Qy	6	SEIW 9								
Best Local Similarity	Db	2	SSIW 5								
Matches 3 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;											
RESULT 7											
A43129	Qy	7	ELW 9								
neuropeptide GNFRPamide - tapeworm (Moniezia expansa)	Db	4	ELW 6								
C;Species: Moniezia expansa											
C;Accession: A43129											
C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004											
Query Match	Qy	7	ELW 9								
Best Local Similarity	Db	4	ELW 6								
Matches 3 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;											
RESULT 8											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: S05002											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 5											
S05002	Qy	7	ELW 9								
corazonin - American cockroach	Db	4	ELW 6								
C;Species: Periplaneta americana (American cockroach)											
C;Accession: S05002											
C;Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004											
Query Match	Qy	7	ELW 9								
Best Local Similarity	Db	4	ELW 6								
Matches 3 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;											
RESULT 6											
PT0519	Qy	6	SEIW 9								
T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)	Db	2	SSIW 5								
C;Species: Mus musculus (house mouse)											
C;Accession: PT0519											
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997											
Query Match	Qy	6	SEIW 9								
Best Local Similarity	Db	2	SSIW 5								
Matches 3 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;											
RESULT 7											
A43129	Qy	7	ELW 9								
neuropeptide GNFRPamide - tapeworm (Moniezia expansa)	Db	4	ELW 6								
C;Species: Moniezia expansa											
C;Accession: A43129											
C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004											
Query Match	Qy	7	ELW 9								
Best Local Similarity	Db	4	ELW 6								
Matches 3 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;											
RESULT 8											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 9											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 10											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 11											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 12											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 13											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 14											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								
Best Local Similarity	Db	1	GSFF 4								
Matches 3 ; Conservative 0 ; Mismatches 1 ; Indels 0 ; Gaps 0 ;											
RESULT 15											
A41117	Qy	2	GSFF 5								
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)	Db	1	GSFF 4								
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)											
C;Accession: A41117											
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004											
Query Match	Qy	2	GSFF 5								

A;Cross-references: UNIPROT:Q7LZ27
C;Keywords: carboxylic ester hydrolase

Query Match Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 SELW 9
Db 2 AEMW 5 .

RESULT 9

S36850 19 heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999

R;Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl
A;Reference number: S25024
A;Accession: S36850
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-9 <JAC>
A;Cross-references: EMBL:X67387; NID:g50113; PIDN:CAA47799_1; PID:e51594; PID:91333871

Query Match Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GSFF 5
Db 6 GSYF 9

RESULT 10

S07241 Litoria - Rohde's leaf frog
C;Species: Phyllomedusa rohdei (Rohde's leaf frog)
C;Date: 12-Feb-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004

R;Barra, D.; Falconieri Ersperer, G.; Simmaco, M.; Bossa, F.; Melchiorri, P.; Ersperer,
PEBS Lett. 53:55-56, 1985
A;Title: Rohdeia litoria: a new Peptide from the skin of Phyllomedusa rohdei.
A;Reference number: S07241; PMID:85127560; PMID:3838283
A;Accession: S07241
A;Molecule type: protein
A;Residues: 1-9 <BAR>
A;Cross-references: UNIPROT:PO8946
C;Superfamily: gastrin-releasing peptide
C;Keywords: amidated carboxyl end; blocked amino end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;9/Modified site: amidated carboxyl end (Met) #status experimental

Query Match Score 18; DB 2; Length 9;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 EIWTs 11
Db 1 QIWT 5

RESULT 11

C41946 T-cell receptor gamma chain (1t.60) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999

R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
S33300

Mol. Cell. Biol. 11, 5902-5909, 1991
A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A;Reference number: A41946; MUID:92049316; PMID:1658619
A;Accession: C41946
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-10 <NHE>
C;Keywords: T-cell receptor

Qy 5 FSBLWTS 11
Db 1 YCAVNS 7

RESULT 12

S53789 neuropept.de Pec-HRTH - Platypleura capensis
C;Species: Platypleura capensis
C;Accession: S53789
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
R;Gaede, G.; Janssens, M.P.E.
Biol. Chem. Hoppe-Seyler 375, 803-809, 1994
A;Title: Cicadas contain novel members of the AKH/RPCH family peptides with hypertrehaloseamide-like activity
A;Reference number: S53789; MUID:95225985; PMID:7710694
A;Accession: S53789
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Cross-references: UNIPROT:Q7M465
C;Keywords: blocked amino end; blocked carboxyl end

Query Match Score 18; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 FSBLW 9
Db 4 FSPSW 8

RESULT 13

LFTWWE probable trpEG leader peptide - Thermus aquaticus
C;Species: Thermus aquaticus
C;Accession: S03315
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999
R;Sato, S.; Nakada, Y.; Kanaya, S.; Tanaka, T.
Biochim. Biophys. Acta 950, 303-312, 1988
A;Title: Molecular cloning and nucleotide sequence of *Thermus thermophilus* HB8 trpE and
A;Reference number: S03315; MUID:89000781; PMID:2844259
A;Accession: S03315
A;Molecule type: DNA
A;Residues: 1-11 <SAT>
A;Cross-references: EMBL:X07744; NID:g48261; PIDN:CAA30565_1; PMID:g48262
A;Note: the source is designated as *Thermus thermophilus* HB8
C;Genetics:
A;Gene: trpL
C;Superfamily: probable trpEG leader peptide

Query Match Score 18; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 3.3e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 SELW 9
Db 5 SALW 8

RESULT 14

probable substance P - smaller spotted catshark
 C;Species: Scyliorhinus canicula (smaller spotted catshark, smaller spotted dogfish)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S33300

R;Waugh, D.; Wang, Y.; Hazon, N.; Balment, R.J.; Conlon, J.M.

Eur. J. Biochem. 214, 469-474, 1993

A;Title: Primary structures and biological activities of substance-P-related peptides from

A;Reference number: S33300 ; MTRD:93292508 ; PMID:7655693

A;Accession: S33300

A;Molecule type: protein

A;Residues: 1-11 <WAT>

A;Cross-references: UNIPROT:P41333

A;Experimental source: brain

C;Function:

A;Description: may play a physiological role in the regulation of cardiovascular and gas

A;Note: substance P is derived by post-translational processing of proprotachykinin A

C;Keywords: amidated carboxyl end; neuropeptide; tachykinin

F;8/Modified site: amidated carboxyl end (Met) #status predicted

Query Match Score 18; Score 18;

Best Local Similarity 75.0%; Pred. No. 3.3e+03; Length 11;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSFF 5

 | |

 5 QFFF 8

RESULT 15

JS0315

Leucokinin V - Madeira cockroach

C;Species: Leucophaea maderae (Madeira cockroach)

C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C;Accession: JS0315

R;Holman, G.M.; Cook, B.J.; Nachman, R.J.

Comp. Biochem. Physiol. C 88, 27-30, 1987

A;Title: Isolation, primary structure, and synthesis of leucokinins V and VI: myotropic

A;Reference number: JS0315

A;Accession: JS0315

A;Molecule type: protein

A;Residues: 1-8 <HOL>

A;Cross-references: UNIPROT:P19987

C;Comment: Leucokinins, a family of cephalomyotrop peptide, stimulate contractile act

C;Keywords: amidated carboxyl end; cephalomyotrop peptide

F;8/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match Score 17.5; Score 17.5;

Best Local Similarity 62.5%; Pred. No. 2.8e+05; Length 8;

Matches 5; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 2 GSFFSEIW 9

 | | | |

 1 GSGFSS-W 7

Search completed: April 27, 2005, 15:30:31
 Job time : 38 secs

Scoring table:	BLOSUM62						
Gapop:	10.0 , Gapext 0.5						
Searched:	1612378 seqs, 512079187 residues						
Total number of hits satisfying chosen parameters:	3223						
Minimum DB seq length:	0						
Maximum DB seq length:	11						
Post-processing:	Minimum Match 0% Maximum Match 100%						
Database :	UniProt_03; * 1: uniprot_sprot: 2: uniprot_trembl: *						
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES							
Result No.	Score	Query	Match	Length	DB	ID	Description
-	-	-	-	-	-	-	-
1	24	40.0	11	2	077895		077895 oreochromis
2	24	40.0	11	2	077896		077896 oreochromis
3	23	38.3	10	2	P92576	bipes bipes	P92576 bipes bipes
4	23	38.3	11	2	P85337	lactobacillus	P85337 lactobacillus
5	21	35.0	9	2	Q95953	homo sapien	Q95953 homo sapien
6	20	33.3	10	2	Q6LA62	homo sapien	Q6LA62 homo sapien
7	20	33.3	11	1	CA42_LITCI		CA42_LITCI
8	20	33.3	11	1	CORZ_PERAM		CORZ_PERAM
9	20	33.3	11	1	077894	periplaneta americana	077894 oreochromis
10	20	33.3	11	2	077898	oreochromis	077898 oreochromis
11	19	31.7	6	1	Q65CG7	sinaloa tom	Q65CG7 sinaloa tom
12	19	31.7	8	2	FARP_MONEX		FARP_MONEX
13	19	31.7	8	2	Q99MNO	mus musculus	Q99MNO mus musculus
14	19	31.7	8	2	Q71Z27	naja oxiana	Q71Z27 naja oxiana
15	19	31.7	10	2	Q9TR47	bos taurus	Q9TR47 bos taurus
16	19	31.7	10	2	Q8SHC6	furcifer beauforti	Q8SHC6 furcifer beauforti
17	19	31.7	11	2	Q9UC46	homo sapien	Q9UC46 homo sapien
18	18	30.0	9	1	L1TR_PHYRO	phyllomedusa	P08946 phyllomedusa
19	18	30.0	9	2	Q9h3Y3	homo sapien	Q9h3Y3 homo sapien
20	18	30.0	9	2	Q8H9Z1	cyanophage	Q8h9z1 cyanophage
21	18	30.0	9	2	Q90350	gb virus c	Q90350 gb virus c
22	18	30.0	10	1	AKHX_LOCM1	locusta migratoria	P81626 locusta migratoria
23	18	30.0	10	1	Q7M465	platypyleura	Q7m465 platypyleura
24	18	30.0	10	2	Q8SHB1	rhampholeon	Q8shb1 rhampholeon
25	18	30.0	10	2	Q8SHB4	furcifer velezensis	Q8shb4 furcifer velezensis
26	18	30.0	10	2	Q8SHB7	furcifer valenciennesi	Q8shb7 furcifer valenciennesi
27	18	30.0	10	2	Q8SHC0	furcifer labordi	Q8shc0 furcifer labordi
28	18	30.0	10	2	Q8SHC3	furcifer labordi	Q8shc3 furcifer labordi
29	18	30.0	11	1	LPW_THETH	thermus thermophilus	P05624 thermus thermophilus
30	18	30.0	11	1	TRNA_SCYCA	scyllothrin	P41333 scyllothrin
31	18	30.0	11	2	Q9UELO	homo sapien	Q9uelo homo sapien

RESULT 1							
077895							
ID	077895						
AC	077895;						
DT	01-NOV-1998	(TREMBLrel.	08,	Created)			
DT	01-NOV-1998	(TREMBLrel.	08,	Last sequence update)			
DT	01-DEC-2001	(TREMBLrel.	19,	Last annotation update)			
DB	MHC class II B locus 12	(Fragment).					
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; Actinopterygii; Neopterygii; Teleostei; Euteleoste;						
OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Oreochromis.						
OX	NCBI_TaxID=8128;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	Medline=9815113; PubMed=9649539;						
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,						
RA	Figueiro P., Sultmann H., Klein J.;						
RT	"Linkage relationships and haplotype polymorphism among cichlid MHC genes II B loci."						
RT	Genetics 149:1527-1537(1998).						
RL	EMBL; AF050005; AAC134.1; -.						
DR	NON_TER	1	1				
FT	NON_TER	1	1				
SQ	SEQUENCE	11 AA;	1367 MW;	3F47C9EA772045A3 CRC64;			
Query Match	40.0%						
Best Local Similarity	50.0%						
Matches	4;	Conservative	2;	Mismatches	2;	Indels	0;
Qy	4 PFSELMTS 11						
Db	3 FWSILWVA 10						
RESULT 2							
077896							
ID	077896						
AC	077896;						
DT	01-NOV-1998	(TREMBLrel.	08,	Created)			
DT	01-NOV-1998	(TREMBLrel.	08,	Last sequence update)			
DT	01-DEC-2001	(TREMBLrel.	19,	Last annotation update)			
DB	MHC class II B locus 12	(Fragment).					
OS	Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butelostomi; Actinopterygii; Neopterygii; Teleostei; Euteleoste;						
OC	Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Oreochromis.						
OX	NCBI_TaxID=8128;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RX	Medline=9815113; PubMed=9649539;						
RA	Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,						

RA Figueiroa F.; Sultmann H.; Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 RT Class II B loci.";
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050006; AAC1345..1; -.
 PT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;
 Query Match Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0; Gaps 0;
 Qy :|:|||:
 Db 3 FWSMLW 9

RESULT 3
 P92576 PRELIMINARY; PRT; 10 AA.
 ID P92576;
 AC P92576;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Cytochrome c oxidase subunit I (Fragment).
 GN Name=COI;
 OS Biporus (Baja worm lizard).
 OC Mitochondrion.
 EUkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Lepidosauria; Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
 NCBI_TaxID=52188;
 RN [1] -
 RP SEQUENCE FROM N.A.; PubMed=900757;
 RX MEDLINE=97153826; PubMed=900757;
 RA Macey J.R.; Larson A.; Ananjeva N.B.; Fang Z.; Papenfuss T.J.;
 RT "Two novel gene orders and the role of light-strand replication in
 rearrangement of the vertebrate mitochondrial genome.";
 RL Mol. Biol. Evol. 14:91-104(1997).
 RN [2]
 RP SEQUENCE FROM N.A.; PubMed=900751;
 RX MEDLINE=97153820; PubMed=900751;
 RA Macey J.R.; Larson A.; Ananjeva N.B.; Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 DR BMBL; UT1335; AAB48271.1; -.
 DR PIR; T13838; T13838.
 DR GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1176 MW; 5B3580C9D5A41A7 CRC64;
 Query Match Score 23; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.7e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Gaps 0;
 Qy :|:|||:
 Db 4 TRSFFS 9

RESULT 4
 P83537 PRELIMINARY; PRT; 11 AA.
 ID P83537;
 AC P83537;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB Unknown protein from 2D-page (Fragment).
 OS Lactobacillus sanfranciscensis (Lactobacillales; Lactobacillaceae);
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 Lactobacillus

OX NCBITaxID=1625;
 RN [1] -
 RP SEQUENCE AND INDUCTION.
 RC STRAIN=DSM 20451;
 RX PubMed=12112860;
 RX DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
 RA Drews O.; Weiss W.; Reil G.; Parlar R.; Wait R.; Goerg A.;
 RT "High pressure effects step-wise altered protein expression in
 Lactobacillus sanfranciscensis.";
 RL Proteomics 2:765-774(2002).
 CC !- INDUCTION: By elevated hydrostatic pressure.
 CC -: MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 CC protein is: 65 kDa.
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1249 MW; D96CC231B771ADD9 CRC64;

RESULT 5
 095953 PRELIMINARY; PRT;
 ID 095953
 AC 095953
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DB Galactocerebrosidase (EC 3.2.1.46) (Fragment).
 GN Name=GALC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Lulli L.; Torchiana E.; Finocchiaro G.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U77631; ADD1526.1; -.
 DR GO:0004336; F:Galactosylceramidase activity; IEA.
 DR GO:0016798; F:Hydroxide activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; F:Carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2ADC2C699C8 CRC64;

RESULT 6
 Q6LA62 PRELIMINARY; PRT;
 ID Q6LA62
 AC Q6LA62
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DB Amiloride-sensitive epithelial sodium channel gamma subunit
 (Fragment).
 GN Name=SCNN1G;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]

RP SEQUENCE FROM N.A.; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
 RX MEDLINE=96421599;

RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;

RT "Genomic organization and the 5' flanking region of the gamma subunit
 of the human amiloride-sensitive epithelial sodium channel.";

J. Biol. Chem. 271:26062-26066 (1996).
 RN [2]

RP SEQUENCE FROM N.A.; PubMed=9654208;
 RX MEDLINE=98316780;

RA Ludwig M., Bolkenius U., Wickert L., Marynen P., Bidlingmaier F.;
 RT "Structural organization of the gene encoding the alpha-subunit of the
 human amiloride sensitive epithelial sodium channel.";

RL Hum. Mol. Genet. 10:576-581 (1998).

DR EMBL:292982; CAB:07506.1; -;

DR GO:GO:0005216; P:ion channel activity; IEA.

KW Ionic channel.

FT NON-TER 1 1
 FT NON-TER 10 10
 SQ SEQUENCE 10 AA; 1157 MW; DBAFF83733805A2 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 9.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Gaps 0;
 Indels 0;

Qy 3 SFPSSELW 9
 Db 1 SVVSEKRN 7

RESULT 7
 CA42_LITCI CA42_LITCI STANDARD: PRT; 11 AA.

AC P82052; [1]

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Caeerulein 4.2/4.2Y4.

OS Litoria citropa (Australian blue mountains tree frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Rilyidae;

OC Peleodryadinae; Litoria.

NCBI_TaxID=94770; [1]

RP SEQUENCE, AND MASS SPECTROMETRY.

RC TISSUE=Skin secretion;

RX MEDLINE=983157701; PubMed=10589099;

RA Wabnitz P.A., Bowie J.H., Tyler M.J.;

RT "Caeerulein-like Peptides from the skin glands of the Australian blue
 mountains tree frog Litoria citropa. Part 1. Sequence determination
 using electrospray mass spectrometry";

RL Rapid Commun. Mass Spectrom. 13:2458-2502 (1999).

CC "- FUNCTION: Hypotensive neuropeptide (Probable).
 CC "- SUBCELLULAR LOCATION: Secreted.

CC "- TISSUE SPECIFICITY: Skin dorsal glands.

CC "- ISOTYPE: Isoform 4.2Y4 differs from isoform 4.2 in not being sulfated.
 CC "- NOTE=Ref. 1.

CC "- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

DR InterPro; IPR001651; Gastrin.

DR PROSITE; PS00259; GASTRIN; FALSE_NEG.

KW Amidopeptidase; Amphibian defense peptide; Direct protein sequencing;

KW Hypotensive agent; Pyrrolidone carboxylic acid; Sulfation.

FT MOD_RES 1 1
 FT MOD_RES 4 4
 FT MOD_RES 11 11

FT Pyrrolidone carboxylic acid.

FT Phenylalanine amide.

SQ SEQUENCE 11 AA; 1344 MW; 10DAB94F5B861BB CRC64;

Query Match 33.3%; Score 20; DB 1; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGSFP 5 Db 5 TGSHF 9	RESULT 8 CORZ_PERAM ID CORZ_PERAM STANDARD; PRT; 11 AA. AC P11496; DT 01-OCT-1989 (Rel. 12, Created) DT 01-FEB-1994 (Rel. 28, Last sequence update) DT 05-JUL-2004 (Rel. 44, Last annotation update) DE Corazonin. OS Periplaneta americana (American cockroach). OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea; OC Blattidae; Periplaneta. RN [1] NCBITaxID=6978; RP SEQUENCE.
Qy 1 TGSFP 5 Db 5 TGSHF 9	RC TISSUE=Corpora cardiaca; RX MEDLINE=89325572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6; RA Veensstra J.A.; RT "Isolation and structure of corazonin, a cardioactive peptide from the American cockroach."; RL FEBS Lett. 250:231-234 (1989). CC "- FUNCTION: Cardioactive peptide. Corazonin is probably involved in the physiological regulation of the heart beat. CC "- SUBCELLULAR LOCATION: Secreted. DR PIR: S05002; S05002. KW Amidation; Direct protein sequencing; Neuropeptide; KW Pyrrolidone carboxylic acid. FT MOD_RES 1 1 FT MOD_RES 11 11 SQ SEQUENCE 11 AA; 1387 MW; C7CF32D641SAB46 CRC64;
Qy 1 TGSFP 5 Db 5 TGSHF 9	Query Match 33.3%; Score 20; DB 1; Length 11; Best Local Similarity 42.9%; Pred. No. 1e+04; Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 5 FSELWTS 11 Db 5 YSRGWTN 11	Qy 5 FSELWTS 11 Db 5 YSRGWTN 11
Qy 5 FSELWTS 11 Db 5 YSRGWTN 11	RESULT 9 O77894 PRELIMINARY; PRT; 11 AA. ID O77894 AC O77894; DT 01-NOV-1998 (TREMBLrel. 08, Created) DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update) DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update) DE MHC class II B locus 12 (Fragment). OS Oreochromis niloticus (Nile tilapia). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterigii; Teleostei; Euteleostei; Neoteleostei; OC Cichlidae; Oreochromis. RN [1] NCBITaxID=8128;
Qy 5 FSELWTS 11 Db 5 YSRGWTN 11	RP SEQUENCE FROM N.A.; RX MEDLINE=98315113; PubMed=9649539; RA Malaga-Trillo B., Zaleska-Rutczynska Z., McAndrew B., Vincek V., RA Figueiroa F., Sultmann H., Klein J.; RT "Linkage relationships and haplotypes polymorphism among cichlid MHC class II B loci."; RT Class II B loci.; RL EMBL; AF050044; AAC1341.1; -;
Qy 5 FSELWTS 11 Db 5 YSRGWTN 11	FT NON-TER 1 1 FT NON-TER 11 11 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;

Query Match 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FFSELW 9
 Db 3 FWSIVW 8

Db 4 SFWVFLFS 11

RESULT 10

PPRPMONEX STANDARD; PRT; 6 AA.

AC P41966; DT 01-NOV-1995 (Rel. 32, Created)
 AC 077898; PRELIMINARY; PRT; 11 AA.
 DT 01-NOV-1998 (TREMBLrel. 08, Created)
 AC 077898; PRELIMINARY; PRT; 11 AA.
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DB MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile Tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Cestoda; Bucestoda;
 OC Actantheropterygi; Neopterygi; Teleostei; Neoteleosteoi; Osteoleptidae; Osteogasteridae; Osteomorpha; Perciformes; Labroidei; Cichlidae; Oreoichromis.
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=9649539;
 RX MEDLINE=93312289; PubMed=8323531;
 RA Malaga-Trillo E.; Zaleska-Rutczynska Z.; McAndrew B.; Vincent V.; Piquero F.; Sultmann H.; Klein J.; RT "Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci."
 RL Genetics 149:1527-1537(1998).
 FT EMBL; AF050008; AAC41347.1; -.
 FT NON_TER 1 1
 FT SEQENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;
 SQ

Query Match 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FFSELW 9
 Db 3 FWSIVW 8

Db 4 SFWVFLFS 11

RESULT 11

PPRPMONEX STANDARD; PRT; 8 AA.

AC Q99MNO; DT 01-JUN-2001 (TREMBLrel. 17, Created)
 AC Q99MNO; DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 AC Q65CG7; PRELIMINARY; PRT; 11 AA.
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DB Transcriptional activator (Fragment).
 GN Name=AC2;
 OC Sinaloa tomato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OC NCBI_TaxID=71186;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NI1;
 RA Rojas A.; Kvarnheiden A.; Rodriguez D.; Valkonen J.P.T.; RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in Nicaragua."
 RT EMBL; AJ508781; CAD48523.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1356 MW; 861BC90602D379DS CRC64;
 Query Match 33.3%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+04; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SFPELWMT 10

RESULT 14

Q7LZZ7 PRELIMINARY; PRT; 8 AA.

ID Q7LZZ7; PRELIMINARY; PRT; 8 AA.

AC Q7LZZ7; PRELIMINARY; PRT; 8 AA.

DT 01-MAR-2004 (T-EMBLrel. 26, Created)

DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DB Acetylcholinesterase (EC 3.1.1.7), venom (Fragment).

OS Naja oxiana (Central Asian cobra) (Oxus cobra).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Elapidae; Elapinae; Naja.

OX NCBI_TaxID=8657;

RN [1]

RP SEQUENCE.

RX MEDLINE=91296772; PubMed=20680931;

RA Kreienkamp H.J., Weisse C., Raba R., Aviksaar A., Hucho F.;

RT "Anionic subsites of the catalytic center of acetylcholinesterase from Torpedo and from cobra venom."

RT Proc. Natl. Acad. Sci. U.S.A. 88:6117-6121(1991).

RL PIR; A41117; A11117.

DR GO:0003990; F:acetylcholinesterase activity; IEA.

PT NON-TER 1 1

FT 8 8

SQ SEQUENCE 8 AA; 918 MW; 7F57645376B1DD8 CRC64;

Query Match Score 19; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy :|:

Db 6 SELW 9

7 EMW 5

RESULT 15

Q9TR47 PRELIMINARY; PRT; 10 AA.

ID Q9TR47; PRELIMINARY; PRT; 10 AA.

AC Q9TR47; PRELIMINARY; PRT; 10 AA.

DT 01-MAY-2000 (T-EMBLrel. 13, Created)

DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)

DB Amphoterin homolog (Fragment).

OS Bos taurus (Bovine).

OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos

NCBI_TaxID=9913;

RN [1]

RP SEQUENCE.

RX MEDLINE=96029671; PubMed=7592757; DOI=10.1074/jbc.270.43.25752;

RA Hori O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,

RA Nagashima M., Lundh B.R., Vijay S., Nitzeck D.

RT "The receptor for advanced glycation end products (RAGE) is a cellular binding site for amphoterin. Mediation of neurite outgrowth and co-expression of rage and amphoterin in the developing nervous system.";

RL J. Biol. Chem. 270:25752-25761(1995).

SQ SEQUENCE 10 AA; 1163 MW; 28E5034453769B18 CRC64;

Query Match Score 19; DB 2; Length 10;

Best Local Similarity 40.0%; Pred. No. 1.4e+04;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy :|:

Db 7 ELWTS 11

4 EMWNN 8

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target HGBV. The method is used for detecting target HGBV nucleic acid in the test sample suspected of containing HGBV and for characterisation of newly ascertained etiological agent of non-A, non-B, non-C, non-D and non-E hepatitis causing agents collectively termed as hepatitis GB virus. AAA55270 to AAA55489 and AAB08985 to AAB09480 represent nucleotide and protein sequences used in the exemplification of the present invention. (Updated on 06-AUG-2003 to correct OS field.)

SQ Sequence 8 AA;

Query Match Score 34; DB 3; Length 8;
Best Local Similarity 56.7%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 5 FSELWTS 11

Db 1 FSHLWTS 7

Db Sequence 8 AA;

Db ADK09671

ID ADK09671 standard; peptide; 10 AA.

XX AC ADK09671;

XX DT 06-MAY-2004 (first entry)

XX DE Human papillomavirus peptide #1726.

XX KW pathogenic virus; alternative reading frame; antigenic determinant;

XX virucide; vaccine; therapeutic agent; infection; HPV.

XX OS Human papillomavirus.

XX PS Human papillomavirus.

XX PN WO2004011650-A2.

XX PD 05-FEB-2004.

XX PF 24-JUL-2003; 2003WO-EP0008112.

XX PR 24-JUL-2002; 2002AT-00001124.

XX PR 11-JUL-2003; 2003EP-00450171.

XX PA (INTE-) INTERCELL AG.

XX PI Mattner F, Schmidt W, Habel A;

XX DR WPI; 2004-169243/16.

XX PS Claim 18; Page 187; 220pp; English.

XX XX New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.

XX XX This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the invention.

XX SQ Sequence 10 AA;

XX PS Query Match Score 31; DB 8; Length 10;

XX PS Best Local Similarity 51.7%; Pred. No. 96;

XX CC Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

XX CC Qy 3 SFFSEWT 10

XX CC Db 1 SFFSRTWS 8

XX CC RESULT 4 ABR46515

XX ID ABR46515 standard; peptide; 6 AA.

XX AC ABR46515;

XX DT 10-JUN-2003 (first entry)

XX DE Staphylococcus aureus CHIPS-related peptide #1705.

XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;

XX SQ 3 SFSEWT 10

XX Qy

formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell; inflammation; cardiovascular disease; central nervous system disease; gastrointestinal disease; skin disease; genitourinary disease; joint disease; respiratory disease; HIV infection; antiinflammatory; cardiant; cerebroprotective; neuroprotective; nootropic; dermatological; gynecological; immunosuppressive; anti-HIV.

XX OS *Staphylococcus aureus*.
OS Synthetic.

XX PN WO2003006048-A1.
XX PD 23-JAN-2003.
XX PP 11-JUL-2001; 2001WO-EP008004.
XX PR 11-JUL-2001; 2001WO-EP008004.
PA (JARI-) JARI PHARM BV.

PI Van Kessel CPM, Gosselaar-De Haas CJJC, Kruijzer JAW;
PT Van Strijp JAG;

XX WPI: 2003-256333/25.
PT Combination of peptides derived from chemotaxis inhibiting protein from *Staphylococcus aureus* (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.

XX Disclosure; Page 17; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR7385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from *Staphylococcus aureus*. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (CsAR) and/or formylated peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic inflammation reactions. The diseases or disorders include cardiovascular diseases, skin diseases, genitourinary diseases, joint diseases, respiratory diseases and HIV infection.

Sequence 6 AA;

Query Match Score 30; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FFFELW 9
Db 1 FFFELW 6

Sequence 6 AA;

Query Match Score 30; DB 6; Length 6;
Best Local Similarity 83.3%; Pred. No. 1.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FFFELW 9
Db 1 FFFELW 6

Query Match Score 30; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFPSLW 9
Db 1 GVFFTNIW 8

Sequence 9 AA;

Query Match Score 30; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFPSLW 9
Db 1 GVFFTNIW 8

RESULT 6
AAW37198 ID AAW37198 standard; peptide; 10 AA.
XX AC AAW37198;
XX DT 20-JUL-1998 (First entry)
XX FH Homo sapiens.
XX Key Location/Qualifiers
FT 1
FT /note= "N-terminal acetyl; Sulphydryl side-chain linked to 6-acryloyl-2-(dimethylamino) naphthalene"
AC AAW2493;
XX DT Modified-site 10
XX FT FT
XX PN WO9801467-A2.
XX PR 15-JAN-1998.
XX PD 04-JUL-1997;
XX PR 05-JUL-1996;
XX PR 07-APR-1997;
XX PA (NOV) NOVARTIS AG.
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX PD 20-OCT-1998.

XX XX XX PR 15-AUG-1994; 94US-00290268.
XX XX PR 15-AUG-1994; 94US-00290268.
PA (GENE-) GENELABS DIAGNOSTICS PTE LTD.
XX PI Chan L, Guan M;
XX DR WPI: 1998-582552/49.
XX PT Dengue virus peptide antigens - especially for diagnosis of dengue virus infection.
XX PS Example 1; Col 17; 21pp; English.
XX CC AAW72456 to AAW72570 represent peptide fragments from the dengue virus type-2 Glycoprotein NS1, which was used in an example from the present invention for an epitope mapping assay. The invention has developed peptide antigens consisting of fragments of the dengue virus NS1 protein. The peptide antigens can be used for the diagnosis of dengue virus infection by detection of antibodies to the virus, especially in an assay comprising attaching the antigen to a solid support, contacting a serum sample with the support, and detecting bound antibodies with a labelled anti-human antibody or used for preparing vaccines against dengue virus infection.
XX SQ Sequence 9 AA;
XX Query Match Score 30; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX Qy 2 GSFFPSLW 9
Db 1 GVFFTNIW 8
XX AC AAW37198;
XX DT 20-JUL-1998 (First entry)
XX FH Homo sapiens.
XX Key Location/Qualifiers
FT 1
FT /note= "N-terminal acetyl; Sulphydryl side-chain linked to 6-acryloyl-2-(dimethylamino) naphthalene"
AC AAW2493;
XX DT Modified-site 10
XX FT FT
XX PN WO9801467-A2.
XX PR 15-JAN-1998.
XX PD 04-JUL-1997;
XX PR 05-JUL-1996;
XX PR 07-APR-1997;
XX PA (NOV) NOVARTIS AG.
XX PA (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
XX PD 20-OCT-1998.

PI Lane D, Boettger V, Boettger A, Picklesley S, Hochkeppel H;
 PI Garcia-Echeverria C, Chene P, Furet P;
 XX DR; 1998-100996/09.

XX Compounds binding to MDM2 protein and inhibit its interaction with p53 -
 PT peptide derivative capable of binding to a human
 PT oncogenic protein MDM2. The MDM2 binding peptides can specifically
 PT inhibit or block the binding of MDM2 to the human p53 protein, in vitro
 PT or vivo. Inhibit growth or apoptosis in tumour cells comprising a wild-type
 PT p53 and non-elevated levels of MDM2. The peptides may be used to identify
 PT especially MDM2, diagnose disease by measuring levels of MDM2 in blood of
 CC cancer and leukaemia patients and for treatment or prevention of disease
 CC involving p53/MDM2 interactions, especially tumours and viral infections.
 CC The peptides can be administered nasally, rectally, orally or by
 CC injection. By interfering with MDM2/p53 interaction, the peptides can
 CC activate p53 function and accumulation in normal cells. The peptides
 CC which mimic the MDM2 binding site in p53, have a significantly greater
 CC blocking activity compared with wild-type p53

XX Sequence 10 AA;

SQ Query Match 50.0%; Score 30; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSPESELW 9
 :|:|||
 Db 2 GPTESDLW 9

RESULT 7
 ID AAY333139 standard; peptide; 7 AA.

XX AC AAY333139;
 XX DT 16-NOV-1999 (first entry)
 XX DS Rabbit carboxylesterase protein fragment #3.

XX Carboxylesterase; rabbit; tumour cell; chemotherapy; prodrug; recurrence;
 KW disease specific promoter; CRT-11; APC; resection; recurrence;
 KW inhibition; bone marrow cell.

OS Oryctolagus cuniculus.

XX PA (STUD-) ST JUDE CHILDREN'S RES HOSPITAL.
 PN WO9942593-A1.
 XX PD 26-AUG-1999.
 XX PF 12-FEB-1999; 99WO-US003171.
 XX PR 19-FEB-1998; 98US-0075258P.

XX PA Danks MK, Porter PM, Houghton PJ;
 XX DR; 1999-540311/45.

XX PT New carboxylesterase polypeptide for treatment of tumors.

XX PS Example 2; Page 57; 70pp; English.

CC This invention describes a novel rabbit carboxylesterase polypeptide (I)
 CC capable of metabolizing a chemotherapeutic prodrug and its inactive
 CC metabolites into an active drug. The invention also describes a
 CC composition comprising (I) and a disease-specific responsive promoter.
 CC This composition is useful for sensitizing tumor cells to a
 CC chemotherapeutic prodrug (preferably CRT-11 or APC) by transfecting into
 CC tumor cells, and contacting the sensitized cells with a chemotherapeutic
 CC prodrug to inhibit growth of the tumor cells. The composition can also be
 CC administered to the site of tumor resection to inhibit tumor recurrence,
 CC and be administered to bone marrow cells to remove tumor cells. The
 CC products of the invention are useful for identifying drugs that are
 CC inactivated by a carboxylesterase enzyme, and are also useful for
 CC identifying compounds containing COOC ester linkage that are activated
 CC by a carboxylesterase enzyme. This sequence represents a fragment of a
 CC rabbit carboxylesterase which is described in the method of the invention

XX Sequence 7 AA;

SQ Query Match 48.3%; Score 29; DB 2; Length 7;
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SFPSELW 9
 :|:|||
 Db 1 AFPTSELW 7

RESULT 8
 ID AAU93215 standard; peptide; 10 AA.

XX AAU93215;

XX AC AAU93215;

XX DT 02-JUL-2002 (first entry)

XX DE Granulocyte-colony stimulating factor receptor; cytokine;

XX KW G-CSFR; granulocyte-colony stimulating factor; neutrophil proliferation; AIDS;

XX KW haematopoietic growth factor; neutrophil syndrome;

XX KW neutrophil differentiation; acquired immunodeficiency syndrome;

XX KW chemotherapy-induced neutropenia; community acquired pneumonia;

XX KW depressed neutrophil count; immunostimulant

XX Synthetic.

XX OS WO200207676-A2.

XX PN 20000207676-A2.

XX PD 31-JAN-2002.

XX PF 20-JUL-2001; 2001WO-US023046.

XX PR 20-JUL-2000; 2000US-00620091.

XX PA (GLAXO) GLAXO GROUP LTD.

XX PI Cwirla SE, Balu P, Duffin DJ, Piplani S, McEwen-Merrill B;

XX PI Schatz PJ;

XX DR WPI: 2002-329382/36.

XX PT Novel compounds, useful for treating depressed neutrophil count, comprise
 PT peptide chains of approximately 6 to 40 amino acids in length that bind
 PT to granulocyte-colony stimulating factor receptor.

XX PT Claim 3; Page 52; 90pp; English.

XX The invention relates to compounds comprising a peptide chain
 CC approximately 6 to 40 amino acids in length that binds to granulocyte-
 CC colony stimulating factor receptor (G-CSFR). The compounds contain
 CC specific sequences of the generic peptides appearing as AAU9402-AAU79406
 CC and the generic sequences XV₁-XV₂-XV₃-XV₄-XV₅-XV₆ where XV₁ =
 CC E, C, Q, V or Y; XV₂ = E, A, L, M, S, W or Q; XV₃ = K, R or T; XV₄ =
 CC L, A or V; XV₅ = R, A, M, H, E, V, L, G, D, Q or S; XV₆ = E or V; XV₇ =

CC = A or G; and XVII₈ = R, H, G or L) and XVI₁XVII₂XVII₃XVII₄XVII₅
 CC EXVI₁XVII₂XVII₃XVII₄XVII₅ (where XVII₁ = A, E or G; XVII₂ = E, H or D; XVII₃
 CC = R or G; XVII₄ = K, Y, M, N, Q, R, D, I, S or E; XVII₅ = A, S or P;
 CC XVII₆ = E, D, T, Q, K or A; XVII₇ = R, W, K, L, S, A or Q; XVII₈ = R or E
 CC ; associated with depressed neutrophil count e.g. chemotheraphy-induced
 CC neutropaenia, AIDS-induced neutropaenia or community-acquired pneumonia-
 CC induced pneumonia. The compounds are useful as *in vitro* tools for
 CC understanding the biological role of granulocyte-colony stimulating
 CC factor (G-CSF a haematopoietic growth factor and cytokine that stimulates
 CC neutrophil proliferation and differentiation), including evaluation of
 CC many factors thought to influence, and be influenced by, production of
 CC white blood cells, in the development of compounds that bind to G-CSFR,
 CC as reagents for detecting G-CSFR receptor or related receptor on living
 CC cells, fixed cells, in biological fluids, in tissue homogenates or in
 CC activated cell sorting (FACS), Western blotting or enzyme-linked
 CC immunoadsorptive assay (ELISA), in receptor purification or in purifying
 CC cells expressing G-CSFR on the cell surface (or inside permeabilised
 CC cells) as a commercial research reagent for various medical and
 CC diagnostic uses or to treat a disease that would benefit from the ability
 CC to of a compound to mimic the effects of G-CSF *in vivo*. The compounds
 CC bind specifically to G-CSFR and allow for studies of biological
 CC activities mediated by the receptor and for the treatment of diseases,
 CC disorders and conditions that would benefit from activating or
 CC inactivating G-CSFR. The present sequence is a G-CSFR binding peptide of
 the invention

XX Sequence 10 AA;

Query Match 48.3%; Score 29; DB 5; Length 10;
 Best Local Similarity 71.4%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SFWSELW 9
 | : || |
 3 SFWSELW 9

RESULT 9
 ABUJ37125

ID ABUJ37125 standard; peptide; 11 AA.

AC ABUJ37125;

XX DT 08-MAY-2003 (first entry)

XX Rhodopsin related G-protein coupled receptor binding site peptide #1.

XX Compound library; microenvironment; G-protein Coupled Receptor; GPCR;

XX Rhodopsin.

XX Unidentified.

XX PN WO200304147-A2.

XX PR 06-JUL-2001; 2001GB-00016570.

XX PD 16-JAN-2003.

XX (BIOF-) BIOFOCUS PLC.

XX PF 05-JUL-2002; 2002WO-GB003094.

XX DR 2003-221549/21.

XX PI Crossley R, Rose VS, Stevens AP;

XX XX DR WPI;

XX Producing compound library, by generating biological target model using

PT target sequence information, defining microenvironments interacting with

PT ligand and motifs interacting with microenvironment, and assembling

PT motifs.

XX PT Disclosure; Fig 1; 39pp; English.
 XX CC Disclosure; Fig 1; 39pp; English.
 XX CC The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for synthesis. The
 CC novel method is useful to produce compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a
 CC peptide of a G-protein Coupled Receptor (GPCR) relating to Rhodopsin,
 CC which relates to the novel compound library production method of the
 CC invention

XX SQ Sequence 11 AA;

Query Match 48.3%; Score 29; DB 6; Length 11;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ELWTS 11
 | || |
 2 ELWTS 6

RESULT 10

ABR46459

ID ABR46459 standard; peptide; 6 AA.

XX AC ABR46459;

XX DT 10-JUN-2003 (first entry)

XX DE Staphylococcus aureus CHIPS-related peptide #1649.

XX KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5aR;

XX KW formylated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;

XX KW inflammation; cardiovascular disease; central nervous system disease;

XX KW gastrointestinal disease; skin disease; genitourinary disease;

XX KW joint disease; respiratory disease; HIV infection; antiinflammatory;

XX KW cardiot; cerebroprotection; neuroprotective; nootropic; dermatological;

XX KW synecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS OS Synthetic.

XX PN WO2003006048-A1.

XX PD 23-JAN-2003.

XX (JARI-) JARI PHARM BV.

XX WPI; 2003-256333/25.

XX Van Kessel CPM, Gosselaar-De Haas CJ, Kruijtzer JAW;

XX PI Van Strijp JAG;

XX DR WPI; 2003-256333/25.

XX Combination of peptides derived from chemotaxis inhibiting protein from

PT Staphylococcus aureus (CHIPS) having CHIPS activity, useful in

PT prophylaxis and treatment of inflammation, cardiovascular, skin and

PT kidney diseases.

XX PS Disclosure; Page 16; 89pp; English.

XX CC The present invention relates to peptides (ABR44811-ABR47162 and ABR47164

CC -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from

CC Staphylococcus aureus. The peptide fragments are useful in the

CC prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or formylated peptide receptor (FPR) or neutrophils, CC monocytes and endothelial cells or involving acute or chronic CC inflammation reactions. The diseases or disorders include cardiovascular CC diseases, disease of the central nervous system, gastrointestinal CC diseases, skin diseases, genitourinary diseases, joint diseases, CC respiratory diseases and HIV infection

XX Sequence 6 AA;

Query Match Score 28; DB 6; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 FSEELW 9
| : |
Db 1 FFEIW 6

RESULT 11
ID ADR68302 standard; Peptide; 7 AA.

XX ADR68302;
XX
DT 02-DEC-2004 (First entry)

DB Androgen receptor interacting peptide SEQ ID NO:20.
XX androgen receptor binding peptide; androgen receptor interacting peptide;
KW androgen receptor; cyrostatic; gene therapy; prostate cancer.

XX Mammalia.
OS Synthetic.
PN WO2004076473-A2.
XX
PD 10-SEP-2004.
PP 10-FEB-2004; 2004WO-US003744.
XX PR 12-FEB-2003; 2003US-0446955P.
XX PA (KARO-) KARO BIO AB.
XX PI Buehrer BM, Barnett TR;
XX DR 2004-653365/63.

PT New polypeptides that bind to the androgen receptor, useful for PT diagnosing or treating diseases associated with abnormal levels of PT activation of androgen receptor, e.g. prostate cancer, or in biological PT research.

XX Disclosure; SEQ ID NO 20; 46pp; English.

CC The present invention describes a polypeptide that binds to the androgen receptor, or a polypeptide that comprises at least 50% amino acid sequence identity to the polypeptide. Also described: (1) methods of CC analysing the surface conformation of a protein using one or more of the CC polypeptide sequences mentioned above; (2) methods of identifying CC modulators of protein function using one or more of the polypeptide CC sequences mentioned above; (3) a pharmaceutical composition comprising a pharmaceutical carrier and one or more of the polypeptide sequences CC described above; (4) a peptide that binds to the androgen receptor, the CC binding being competitively inhibited by the polypeptide described above; (5) a chimeric protein comprising the above polypeptide and at least a CC portion of a filamentous phage protein, the portion of the filamentous CC phage protein being sufficient for integration of the chimeric protein CC into the coat of phage particles to display the polypeptide; (6) a method of CC filamentous phage displaying the above polypeptide; (7) a method of CC diagnosing a disease in a patient characterised by abnormal levels of CC activation of androgen receptor, comprising providing a sample of body

CC fluid or tissue of the patient, administering a diagnostic amount of the CC pharmaceutical composition described above, and assaying the amount of CC activated androgen receptor in the body fluid or tissue of the patient; CC and (8) a method of treating a patient suffering from a disease CC characterised by abnormal levels of activation of androgen receptor, CC comprising administering to the patient a therapeutic amount of the CC pharmaceutical composition described above, the androgen receptor, CC interacting polypeptide has cytostatic activity, and can be used in gene CC therapy. The composition and methods are useful for diagnosing or CC treating patients suffering from diseases characterised by abnormal CC levels of activation of androgen receptor, such as prostate cancer. They CC may also be used in biological research, as therapeutics or for in vitro CC or in vivo classification of compounds. The present sequence represents CC an androgen receptor interacting peptide, which is used in the gene CC exemplification of the present invention.

XX SQ Sequence 7 AA;

Query Match Score 28; DB 8; Length 7;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SPPSELM 9
| : ||
Db 1 SRPAELW 7

RESULT 12

XX AAY04678 standard; peptide; 9 AA.
ID AAY04678
XX
AC AAY04678;
XX DT 22-JUN-1999 (first entry)
XX DE Peptide #13 encoded by HsdR/M/S gene fragment.
XX KW HsdR; HsdM; HsdS; restriction/modification; bacteriophage; resistance;
KW lactic acid bacterium.
XX AC AAY04678;
XX DT 22-JUN-1999
XX DE Peptide #13 encoded by HsdR/M/S gene fragment.
XX KW HsdR; HsdM; HsdS; restriction/modification; bacteriophage; resistance;
KW lactic acid bacterium.
XX OS Lactococcus lactis.
XX PN FR2767831-A1.
XX PD 05-MAR-1999.
XX PP 02-SEP-1997; 97FR-00010885.
XX PR 02-SEP-1997; 97FR-00010885.

XX PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
XX PI Chopin MC, Clier F, Ehrlich SD, Gautier M, Schouler C;
XX DR 1999-183265/16.
XX PT Bacteriophage resistance mechanism subunit polypeptides - of lactic acid
bacteria, especially Lactobacillus lactis.

XX PS Claim 7; Page 62; 65pp; French.
XX
XX The invention relates to polypeptides that constitute the HsdR, HsdM or HsdS subunit of a R/M [restriction/modification] type Ic bacteriophage CC resistance mechanism active against the phages of lactic acid bacteria, CC especially Lactococcus lactis. Also claimed are fragments of the HsdR, CC HsdM and HsdS gene which encode peptides AAY04666-Y44679. Nucleic acids CC encoding the HsdR, HsdM or HsdS fragment can be used for expression of at CC least one bacteriophage resistance mechanism in a lactic acid bacterium CC XX Sequence 9 AA;

Query Match Score 28; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.8e+06;

XX PF 16-APR-2003; 2003WO-US011935.
 XX PR 17-APR-2002; 2002US-0373686P.
 XX PA (CREA/) CREA R.
 PA (CAPP/) CAPPUCILLI G.
 XX PI Crea R, Cappuccilli G;
 XX DR WPI: 2003-854132/79.
 XX PS Example; Fig 7; 4 opp; English.
 XX This invention relates to a novel method of walk-through mutagenesis of a nucleic acid encoding a polypeptide which comprises synthesising a mixture of oligonucleotides comprising a nucleotide sequence for each target region of a prototype amino acid, where each oligonucleotide contains, at each sequence position in the target region, a prototype nucleotide for synthesis of the prototype amino acid, or a predetermined nucleotide that is required for synthesis of the predetermined amino acid. The method is useful in producing mutant polypeptides in which the overall presence of the predetermined amino acid is limited to one or two positions per mutated polypeptide, leaving the remaining amino acids in the targeted region intact or as close as possible to the prototype sequence. The invention was exemplified using the three complementarity determining regions (CDRs) of the heavy chain of the monoclonal antibody MCPC 603.
 XX SQ Sequence 11 AA;
 Query Match 46.7%; Score 28; DB 7; Length 11;
 Best Local Similarity 44.4%; Pred. No. 3.6e-02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 SFFSELWTS 11
 | : | | : |
 Db 1 SYSSSWSS 9

Search completed: April 27, 2005, 15:26:49
 Job time : 172 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:23:03 ; Search time 42 Seconds (without alignments)

19.551 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFSELWTS 11

Scoring table: BL0SM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 125705

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0% Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents AA:*

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 2: /cgn2_6/_ptodata/1/iaa/5B_COMB.pep:
 3: /cgn2_6/_ptodata/1/iaa/6A_COMB.pep:
 4: /cgn2_6/_ptodata/1/iaa/6B_COMB.pep:
 5: /cgn2_6/_ptodata/1/iaa/_PCTUS_COMBO.pep:
 6: /cgn2_6/_ptodata/1/iaa/_backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	34	56.7	8	4	US-08-469-260A-252	Sequence 252, Appl
2	34	56.7	8	4	US-08-488-446-252	Sequence 252, Appl
3	34	56.7	8	4	US-08-467-344A-252	Sequence 252, Appl
4	34	56.7	8	4	US-08-424-550B-252	Sequence 252, Appl
5	30	50.0	6	1	US-08-424-957-6	Sequence 6, Appl
6	30	50.0	6	3	US-09-035-686-6	Sequence 6, Appl
7	30	50.0	11	1	US-08-424-957-42	Sequence 42, Appl
8	30	50.0	11	3	US-09-035-686-42	Sequence 42, Appl
9	29	48.3	7	4	US-09-595-602B-10	Sequence 10, Appl
10	29	48.3	10	4	US-09-620-001-28	Sequence 28, Appl
11	28	46.7	11	3	US-09-186-950-6	Sequence 6, Appl
12	28	46.7	11	3	US-09-669-271A-6	Sequence 6, Appl
13	28	46.7	11	4	US-09-881-216-6	Sequence 6, Appl
14	27	45.0	6	1	US-08-277-660A-2	Sequence 2, Appl
15	27	45.0	6	1	US-08-424-957-2	Sequence 2, Appl
16	27	45.0	6	3	US-09-035-686-2	Sequence 2, Appl
17	27	45.0	6	4	US-09-081-975-1	Sequence 1, Appl
18	27	45.0	6	4	US-09-028-002B-130	Sequence 130, Appl
19	27	45.0	6	4	US-09-322-384-4	Sequence 4, Appl
20	27	45.0	7	1	US-08-277-660A-27	Sequence 27, Appl
21	27	45.0	7	1	US-08-424-957-15	Sequence 15, Appl
22	27	45.0	7	1	US-08-424-957-19	Sequence 19, Appl
23	27	45.0	7	3	US-09-035-686-15	Sequence 15, Appl
24	27	45.0	7	3	US-09-035-686-19	Sequence 19, Appl
25	27	45.0	10	1	US-08-277-660A-7	Sequence 7, Appl
26	27	45.0	10	1	US-08-424-957-11	Sequence 11, Appl
27	45.0	10	1	US-08-424-957-17	Sequence 18, Appl	

ALIGNMENTS

RESULT 1

US-08-469-260A-252

; Sequence 252, Application US/08469260A
; Patent No. 6515178

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
 APPLICANT: TAMI J. PILOT-MATIAS
 APPLICANT: GEORGE J. DAWSON
 APPLICANT: GEORGE G. SCHLAUDER
 APPLICANT: SURESH M. DESAI
 APPLICANT: THOMAS P. LEARY
 APPLICANT: ANTHONY SCOTT MUERHOF
 APPLICANT: JAMES C. ERICK
 APPLICANT: SHERI L. BULJK
 APPLICANT: ISA K. MUSHAHAR
 TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469,260A
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: POREMBSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527-PC-01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6635
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-469-260A-252
 Query Match 56.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy ||||| 5 FSELWTS 11
 Db 1 FSHLWTS 7

RESULT 2
 US-08-488-446-252
 ; Sequence 252, Application US/08488446
 ; GENERAL INFORMATION:
 ; Paten No. 658898
 ; NUMBER OF SEQUENCES: 716
 ; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 ; CORRESPONDENCE ADDRESS:
 ; APPLICANT: JOHN N. SIMONS
 ; APPLICANT: TAMI J. PILOT-MATIAS
 ; APPLICANT: GEORGE J. DAWSON
 ; APPLICANT: GEORGE G. SCHLAUDER
 ; APPLICANT: SURESH M. DESAI
 ; APPLICANT: THOMAS P. LEARY
 ; APPLICANT: ANTHONY SCOTT MUERHOFF
 ; APPLICANT: JAMES C. ERKER
 ; APPLICANT: SHERI L. BUIJK
 ; APPLICANT: ISA K. MUSHAWAR
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 ; CORRESPONDENCE ADDRESS:
 ; APPLICANT: THOMAS P. LEARY
 ; APPLICANT: JAMES C. ERKER
 ; APPLICANT: SHERI L. BUIJK
 ; APPLICANT: ISA K. MUSHAWAR
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 ; CORRESPONDENCE ADDRESS:
 ; APPLICANT: THOMAS P. LEARY
 ; APPLICANT: JAMES C. ERKER
 ; APPLICANT: SHERI L. BUIJK
 ; APPLICANT: ISA K. MUSHAWAR
 ; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 ; NUMBER OF SEQUENCES: 716
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABATORIES
 ; STREET: 100 ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,344A
 ; FILING DATE: 07-Jun-1995
 ; CLASIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/424,550
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FOREMSKI, PRISCILLA E.
 ; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-6365
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 252:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
 ; US-08-467-344A-252

RESULT 4
 US-08-424-550B-252
 ; Sequence 252, Application US/08424550B
 ; Paten No. 6720166
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; APPLICANT: TAMI J. PILOT-MATIAS
 ; APPLICANT: GEORGE J. DAWSON
 ; APPLICANT: GEORGE G. SCHLAUDER
 ; APPLICANT: SURESH M. DESAI
 ; APPLICANT: THOMAS P. LEARY
 ; APPLICANT: ANTHONY SCOTT MUERHOFF
 ; APPLICANT: JAMES C. ERKER

Query Match 56.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy ||||| 5 FSELWTS 11
 Db 1 FSHLWTS 7

RESULT 3
 US-08-488-446-252
 ; Sequence 252, Application US/08488446
 ; Paten No. 658898
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; APPLICANT: TAMI J. PILOT-MATIAS
 ; APPLICANT: GEORGE J. DAWSON
 ; APPLICANT: GEORGE G. SCHLAUDER
 ; APPLICANT: SURESH M. DESAI
 ; APPLICANT: THOMAS P. LEARY
 ; APPLICANT: ANTHONY SCOTT MUERHOFF
 ; APPLICANT: JAMES C. ERKER

APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BUIK
 APPLICANT: ISA K. MUSHARWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 ZIP: 60064-3500
 COUNTRY: USA

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550B
 FILING DATE:
 CLASSIFICATION: 435435
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMSKI, PRISCILLA E.
 REGISTRATION NUMBER: 33,207
 REFERENCE/DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein

US-08-424-550B-252

Query Match, Score 56.7%; Pred. No. 4.1e+05; Length 8;
 Best Local Similarity 85.7%; 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FSBLWTS 11
 Db 1 FSBLWTS 7

RESULT 5
 US-08-424-957-6
 Sequence 6, Application US/08424957
 ; Patent No. 5770377
 ; GENERAL INFORMATION:
 ; APPLICANT: Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035,686

FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/424,557
 FILING DATE: 19-APR-1995
 APPLICATION NUMBER: US 08/277,660
 FILING DATE: 20-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown

US-09-035-686-6

Query Match 5 FSELW 9 Score 30; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.1e-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9
 Db 2 FSELW 6

COMPUTER READABLE FORM:

RESULT 7
 US-08-424-957-42
 ; Sequence 42, Application US/08424957
 ; GENERAL INFORMATION:
 ; APPLICANT: Picklesley, Steven M.
 ; ATTORNEY/AGENT INFORMATION:
 ; Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Fliehr, Hohbach, Test, Albritton & Herbert
 ; CITY: San Francisco
 ; STATE: California
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/424,957
 ; FILING DATE: 19-APR-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WHD
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; TELEFAX: (415) 398-3249
 ; TELEX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-09-035-686-42

Query Match 5 FSELW 9 Score 30; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9
 Db 5 FSELW 9

RESULT 9
 US-09-595-682B-10
 ; Sequence 10, Application US/09595682B
 ; Patent No. 6800483
 ; GENERAL INFORMATION:
 ; APPLICANT: Danks, Mary K.
 ; ATTORNEY/AGENT INFORMATION:
 ; Peter J.
 ; TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of
 ; Tumor Cells
 ; FILE REFERENCE: SU-0005
 ; CURRENT APPLICATION NUMBER: US/09/595,682B
 ; CURRENT FILING DATE: 2000-01-16
 ; PRIOR APPLICATION NUMBER: 60/075,258
 ; PRIOR FILING DATE: 1998-02-19
 ; PRIOR APPLICATION NUMBER: PCT/US99/03171
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; US-09-595-682B-10

Query Match 5 FSELW 9 Score 30; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSELW 9
 Db 5 FSELW 9

RESULT 8
 US-09-035-686-42
 ; Sequence 42, Application US/09035686
 ; GENERAL INFORMATION:
 ; APPLICANT: Picklesley, Steven M.
 ; ATTORNEY/AGENT INFORMATION:
 ; Lane, David P.
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; NUMBER OF SEQ ID NOS: 30
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 10
 ; LENGTH: 7
 ; TYPE: PRT
 ; ORGANISM: Oryctolagus cuniculus
 ; US-09-035-686-42

Query Match 48.3%; Score 29; DB 4; Length 7;

Best Local Similarity 57.1%; Pred. No. 4.1e+05;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO 6

RESULT 10
 US-09-620-091-28
 Sequence 28, Application US/09620091
 Patent No. 6716811
 GENERAL INFORMATION:
 APPLICANT: CWIRLA, STEVEN E.
 APPLICANT: BALU, PALANI
 APPLICANT: DUFFIN, DAVID J.
 APPLICANT: PIBLANI, SUNIL A.
 APPLICANT: MERRILL, BARBARA MCBOWEN
 APPLICANT: SCHATTZ, PETER JOSEPH
 TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
 FILE REFERENCE: USES
 CURRENT APPLICATION NUMBER: US/09/620,091
 NUMBER OF SEQ ID NOS: 491
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 28
 LENGTH: 10
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 OTHER INFORMATION: Description of Artificial Sequence: Peptide
 SEQ ID NO 28

RESULT 11
 US-09-620-091-28
 Query Match 48.3%; Score 29; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 76;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 SEQ ID NO 6

RESULT 11
 US-09-186-958-6
 Sequence 6, Application US/09186958B
 Patent No. 6238860
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayelle
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 CURRENT APPLICATION NUMBER: US/09/186,958B
 CURRENT FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
 OTHER INFORMATION: binding polypeptide
 SEQ ID NO 6

RESULT 12
 US-09-669-271A-6
 Sequence 6, Application US/09669271A
 Patent No. 6291197
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayelle
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 FILE REFERENCE: Dyax-009 0 US sequence listing
 CURRENT APPLICATION NUMBER: US/09/669,271A
 CURRENT FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: 09/186,958
 PRIOR FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
 OTHER INFORMATION: binding polypeptide
 SEQ ID NO 6

RESULT 13
 US-09-881-276-6
 Sequence 6, Application US/09881276
 Patent No. 6479611
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayelle
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 FILE REFERENCE: DYX-009.0 US-2
 CURRENT APPLICATION NUMBER: US/09/881,276
 CURRENT FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: 09/669,271
 PRIOR FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: 09/186,958
 PRIOR FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Microsoft Word 97
 SEQ ID NO 6

RESULT 14
 US-09-881-276-6
 Sequence 6, Application US/09881276
 Patent No. 6479611
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayelle
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 CURRENT APPLICATION NUMBER: US/09/881,276
 CURRENT FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: 09/669,271
 PRIOR FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: 09/186,958
 PRIOR FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Microsoft Word 97
 SEQ ID NO 6

RESULT 14
 US-09-186-958-6
 Sequence 6, Application US/09186958B
 Patent No. 6238860
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayelle
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 CURRENT APPLICATION NUMBER: US/09/186,958B
 CURRENT FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 6
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
 OTHER INFORMATION: binding polypeptide
 SEQ ID NO 6

RESULT 14
 US-09-277-660A-2
 Sequence 2, Application US/09277660A
 Patent No. 5702908
 GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.

APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/277,660A
 FILING DATE: 20-JUL-1994
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreger, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-60244/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-277-660A-2

Query Match Score 27; DB 1; Length 6;
 Best Local Similarity 80.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 5 FSBLW 9
 | : |
 Db 2 FSDLW 6

RESULT 15

US-08-424-957-2
 / Sequence 2, Application US/08424957
 / Patent No. 5770377
 / GENERAL INFORMATION:
 / APPLICANT: Pickleley, Steven M.
 / APPLICANT: Lane, David P.
 / TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 / NUMBER OF SEQUENCES: 50
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert
 / STREET: Four Embarcadero Center, Suite 3400
 / CITY: San Francisco
 / STATE: California
 / COUNTRY: United States
 / ZIP: 94111-4187
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US 08/424,957
 / FILING DATE: 19-APR-1995
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/277,660

APPLICANT: Lane, David P.
 TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fiehr, Hohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08-424-957-2
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-08-424-957-2

Query Match Score 27; DB 1; Length 6;
 Best Local Similarity 80.0%; Pred. No. 4.1e+05;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 5 FSBLW 9
 | : |
 Db 2 FSDLW 6

Search completed: April 27, 2005, 15:31:20
 Job time : 44 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:29:56 ; Search time 130 Seconds
(without alignments)

28.159 Million cell updates/sec

Title: US-10-088-681-1

Perfect score: 60

Sequence: 1 TGSFSELWTS 11

Scoring table: BLASTM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 197300

Minimum DB seq length: 0

Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
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2: /cgn2_6/picodata/2/pubpaa/PCT_NEW_PUB.pep:
3: /cgn2_6/picodata/2/pubpaa/us06_NEW_PUB.pep:
4: /cgn2_6/picodata/2/pubpaa/us06_PUBCOMB.pep:
5: /cgn2_6/picodata/2/pubpaa/us07_NEW_PUB.pep:
6: /cgn2_6/picodata/2/pubpaa/PCTG_PUBCOMB.pep:
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10: /cgn2_6/picodata/2/pubpaa/us09C_PUBCOMB.pep:
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18: /cgn2_6/picodata/2/pubpaa/us11_NEW_PUB.pep:
19: /cgn2_6/picodata/2/pubpaa/us60_NEW_PUB.pep:
20: /cgn2_6/picodata/2/pubpaa/us60_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	34	56.7	8 US-08-424-550B-252	Sequence 252, App1
2	30	50.0	10 9 US-09-214-371-35	Sequence 35, App1
3	30	50.0	10 9 US-09-114-371-36	Sequence 36, App1
4	29	48.3	10 17 US-10-659-072-28	Sequence 28, App1
5	28	46.7	9 9 US-09-886-724A-35	Sequence 35, App1
6	28	46.7	11 9 US-09-881-276-6	Sequence 6, App1
7	28	46.7	11 15 US-10-417-95A-56	Sequence 56, App1
8	27	45.0	6 9 US-09-214-371-83	Sequence 83, App1
9	27	45.0	6 9 US-09-732-364-4	Sequence 4, App1
10	27	45.0	6 13 US-10-155-059-1	Sequence 1, App1
11	27	45.0	6 15 US-10-609-217-130	Sequence 130, App1
12	27	45.0	6 15 US-10-632-388-130	Sequence 130, App1
13	27	45.0	6 15 US-10-651-723-130	Sequence 130, App1

RESULT
US-08-424-550B-252
Sequence 252, Application US/08/424550B
Publication No. US20020119447A1
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SHUBRESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHRHOFF
APPLICANT: JAMES C. ERICK
APPLICANT: SHERI L. BULUK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSE: Abbott Laboratories D377/AP6D
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREWSKI, PRISCILLA E.

```

REGISTRATION NUMBER: 33,207 ; APPLICANT: Bottger, Angelica
TELECOMMUNICATION INFORMATION: 5527.PC.01 ; APPLICANT: Pickasley, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIORITY APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 36
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Ac-Cys
NAME/KEY: VARIANT
LOCATION: (10)
OTHER INFORMATION: x = Pro-NH2
US-09-214-371-36

Query Match Score 34; DB 8; Length 8;
Best Local Similarity 85.7%; Pred. No. 1.3e+06; Matches 1; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FSFLWTS 11
Db 1 FSHLWTS 7

RESULT 2
US-09-214-371-35
Sequence 35, Application US/09214371B
Patent No. US2010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
APPLICANT: Bottger, Angelica
APPLICANT: Pickasley, Stephen
APPLICANT: Chene, Patrick
APPLICANT: Hochkeppel, Heinz-Kurt
APPLICANT: Garcia-Echeverria, Carlos
APPLICANT: Furet, Pascal
TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIORITY APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 35
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence:peptide
NAME/KEY: VARIANT
LOCATION: (1)
OTHER INFORMATION: X = Ac-Cys (Acrd)
LOCATION: (10)
OTHER INFORMATION: X = Pro-NH2
US-09-214-371-35

Query Match Score 30; DB 9; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.5e+02; Matches 1; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSFFSELW 9
Db 2 GPTFSDLW 9

RESULT 4
US-10-659-207-28
Sequence 28, Application US/10659207
Publication No. US200503759A1
GENERAL INFORMATION:
APPLICANT: CWIRKA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: PIPALANI, SUNIL A.
APPLICANT: MERRILL, BARBARA MCEOWEN
APPLICANT: SCHAVIT, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED USES
TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED USES
FILE REFERENCE: 0300-0014
CURRENT APPLICATION NUMBER: US/10/659,207
CURRENT FILING DATE: 2003-09-09
PRIORITY APPLICATION NUMBER: US/09/620,091
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 28
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-10-659-207-28

Query Match Score 29; DB 17; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.3e+02; Matches 1; Mismatches 1; Indels 0; Gaps 0;
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker
US-09-214-371-36
Sequence 36, Application US/09214371B
Patent No. US2010018511A1
GENERAL INFORMATION:
APPLICANT: Lane, David
APPLICANT: Bottger, Volker

```

9 STEVENS

RESULT 5
US 09-486-734A-35
; Sequence 35, Application US/09486734A

RESULT 5
US-10-417-895A-56
; Sequence 56, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant peptide for third complementarity
OTHER INFORMATION: determining region of Fv region of an
OTHER INFORMATION: immunoglobulin
US-10-417-895A-56

RESULT 6
US-09-486-734A-35
; Sequence 35, Application US/09486734A
; Patent No. US20020164732A1
; GENERAL INFORMATION:
; APPLICANT: Chopin, Marie-Christine
; APPLICANT: Clier, Florence
; APPLICANT: Erlich, S. Dubko
; APPLICANT: Gautier, Michel
; APPLICANT: Schouler, Catherine
; TITLE OF INVENTION: Resistance Mechanisms to IC Type R/M
; TITLE OF INVENTION: Bacteriophages of Lactic Acid Bacteria
FILE REFERENCE: 3333.9/196048
CURRENT APPLICATION NUMBER: US/09/486,734A
CURRENT FILING DATE: 2000-05-03
PRIORITY APPLICATION NUMBER: PCT/FR98/01873
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: PR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hsds subunit
US-09-486-734A-35

Query Match Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GSPESEL 8
Db 2 GSPEKQL 8

RESULT 6
US-09-881-276-6
; Sequence 6, Application US/09881276
; Patent No. US20020031761A1
; GENERAL INFORMATION:
; APPLICANT: Whelihan, E. Payelle
; TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: DYX-009_0 US-2
CURRENT APPLICATION NUMBER: US/09/881,276
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/669,271
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 09/186,958
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Microsoft Word 97
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide
US-09-881-276-6

Query Match Score 28; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 FFSELWTS 11
Db 2 FSDFLW 6

RESULT 7
US-10-417-895A-56
; Sequence 56, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant peptide for third complementarity
OTHER INFORMATION: determining region of Fv region of an
OTHER INFORMATION: immunoglobulin
US-10-417-895A-56

RESULT 8
US-09-214-371B-83
; Sequence 83, Application US/09214371B
; Patent No. US2001001851A1
; GENERAL INFORMATION:
; APPLICANT: Lane, David
; APPLICANT: Bottger, Volker
; APPLICANT: Bottger, Angelica
; APPLICANT: Pickleay, Stephen
; APPLICANT: Chene, Patrick
; APPLICANT: Hochkeppel, Heinz-Kurt
; APPLICANT: Garcia-Echeverria, Carlos
; APPLICANT: Puren, Pascal
; TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
FILE REFERENCE: 4-20937/A/PCT
CURRENT APPLICATION NUMBER: US/09/214,371B
CURRENT FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/EP97/03549
PRIOR FILING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 83
LENGTH: 6
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: peptide, amine
OTHER INFORMATION: acid residues 18-23 of human p53
US-09-214-371B-83

Query Match Score 28; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSEBLW 9
Db 2 FSDFLW 6

RESULT 9
 US-09-732-384-4
 Sequence 4, Application US/09732384
 / GENERAL INFORMATION:
 / APPLICANT: Gu, Jijie
 / TITLE OF INVENTION: Inhibition of p53 Degradation
 FILE REFERENCE: 21508-044
 CURRENT APPLICATION NUMBER: US/09/732,384
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: 60/169,816
 PRIOR FILING DATE: 1999-12-08
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 4
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence:Protein
 OTHER INFORMATION: Fragment not in inhibitory p53 polypeptide
 US-09-732-384-4

Query Match 45.0%; Score 27; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 FSBLW 9
 |:|
 Db 2 FSDLW 6

RESULT 11
 US-10-609-217-130
 / Sequence 130, Application US/10609217
 / Publication No. US20040044188A1
 / GENERAL INFORMATION:
 / APPLICANT: LIU, CHUAN-FA
 / APPLICANT: FEIGE, ULRICH
 / APPLICANT: CHEETHAM, JANET C.
 / APPLICANT: BOONE, THOMAS CHARLES
 / TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 / FILE REFERENCE: A-527
 / CURRENT APPLICATION NUMBER: US/10/609,217
 / PRIOR APPLICATION NUMBER: US/09/428, 082B
 / PRIOR FILING DATE: 1999-10-22
 / PRIOR APPLICATION NUMBER: 60/105,371
 / PRIOR FILING DATE: 1998-10-23
 / NUMBER OF SEQ ID NOS: 1133
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 130
 / LENGTH: 6
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
 US-10-609-217-130

Query Match 45.0%; Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy ~ 5 FSBLW 9
 |:|
 Db 2 FSDLW 6

RESULT 12
 US-10-632-388-130
 / Sequence 130, Application US/10632388
 / Publication No. US20040053845A1
 / GENERAL INFORMATION:
 / APPLICANT: LIU, CHUAN-FA
 / APPLICANT: FEIGE, ULRICH
 / APPLICANT: CHEETHAM, JANET C.
 / APPLICANT: BOONE, THOMAS CHARLES
 / TITLE OF INVENTION: MODIFIED PEPTIDS AS THERAPEUTIC AGENTS
 / FILE REFERENCE: A-527
 / CURRENT APPLICATION NUMBER: US/10/632,388
 / PRIOR APPLICATION NUMBER: US/09/428, 082B
 / PRIOR FILING DATE: 1999-10-22
 / PRIOR APPLICATION NUMBER: 60/105,371
 / PRIOR FILING DATE: 1998-10-23
 / NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Nixon Peabody LLP
 STREET: 101 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/155,059
 FILING DATE: 24-May-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/081,975
 FILING DATE: 12-MAY-1998
 APPLICATION NUMBER: 60/046,207
 FILING DATE: 12-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eisenstein, Ronald I
 REGISTRATION NUMBER: 30,628
 REFERENCE/DOCKET NUMBER: 47400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-345-6054

NUMBER OF SEQ ID NOS: 1133
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 130
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
 US-10-632-388-130

Query Match Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FSEIW 9
 Db 2 FSDLW 6
 ||:||

RESULT 13
 US-10-651-723-130
 Sequence 130, Application US/10651723
 Publication No. US20040057953A1
 GENERAL INFORMATION:
 APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES
 APPLICANT: GUDAS, JEAN MARIE
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527
 CURRENT APPLICATION NUMBER: US/10/651.723
 PRIOR APPLICATION NUMBER: US/09/428,082B
 CURRENT FILING DATE: 2003-08-29
 PRIOR FILING DATE: 1999-10-22
 PRIOR APPLICATION NUMBER: 60/105,371
 PRIOR FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 1133
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 130
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
 US-10-651-723-130

Query Match Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FSEIW 9
 Db 2 FSDLW 6
 ||:||

RESULT 14
 US-10-645-761-130
 Sequence 130, Application US/10645761
 Publication No. US20040071712A1
 GENERAL INFORMATION:
 APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527
 CURRENT APPLICATION NUMBER: US/10/645,761
 PRIOR APPLICATION NUMBER: US/09/428,082B
 CURRENT FILING DATE: 2003-08-18
 PRIOR FILING DATE: 1999-10-22
 PRIOR APPLICATION NUMBER: 60/105,371
 PRIOR FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 1133

RESULT 15
 US-10-666-696-130
 Sequence 130, Application US/10666696
 Publication No. US20040077022A1
 GENERAL INFORMATION:
 APPLICANT: FEIGE, ULRICH
 APPLICANT: LIU, CHUAN-FA
 APPLICANT: CHEETHAM, JANET C.
 APPLICANT: BOONE, THOMAS CHARLES
 APPLICANT: GUDAS, JEAN MARIE
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527A
 CURRENT APPLICATION NUMBER: US/10/666,696
 CURRENT FILING DATE: 2003-09-19
 PRIOR APPLICATION NUMBER: US/09/563,286C
 PRIOR FILING DATE: 2000-05-03
 PRIOR APPLICATION NUMBER: 09/428,082
 PRIOR FILING DATE: 1999-10-22
 PRIOR APPLICATION NUMBER: 60/105,371
 PRIOR FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 1157
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 130
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Mdm/hdm antagonist peptide
 US-10-666-696-130

Query Match Score 27; DB 15; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 FSEIW 9
 Db 2 FSDLW 6
 ||:||

Search completed: April 27, 2005, 15:42:33
 Job time : 131 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:30:37 ; Search time 43 Seconds
(without alignments)

Title: US-10-088-681-2

Perfect score: 67

Sequence: 1 EYGSFFSELWTS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	44.8	10	2 C39191	hypothetical protein
2	28	41.8	9	2 S36850	Ig heavy chain V region
3	25	37.3	12	2 PIR0274	Ig heavy chain CRD
4	24	35.8	7	2 PH1602	Ig H chain V-D-J r
5	22	32.8	9	2 G11946	T-cell receptor ga
6	20	29.9	6	2 B34835	dnaA protein - Pse
7	20	29.9	10	2 T13838	cytochrome-c oxidase
8	20	29.9	11	2 S05002	corazonin - American
9	19	28.4	5	2 B61445	Leu-enkephalin - b
10	19	28.4	5	2 A61445	Met-enkephalin - b
11	19	28.4	6	2 PT0519	T-cell receptor beta
12	19	28.4	6	2 A43129	neuropeptide GFR
13	19	28.4	7	2 A60224	Met-enkephalin-Arg
14	19	28.4	8	2 A41117	acetylcholinesterase
15	19	28.4	10	2 A60410	beta-neoendorphin
16	19	28.4	11	2 PT0520	Ig heavy chain CRD
17	19	28.4	12	2 S152273	thyroglobulin - rat
18	18	26.9	9	2 S07241	litorin - Rohde's
19	18	26.9	10	2 C41946	T-cell receptor ga
20	18	26.9	10	2 S537789	neuropeptide Pec-H
21	18	26.9	11	1 LEFTWIE	probable trpG lea
22	18	26.9	11	1 S41147	chaperonin 10 homo
23	18	26.9	11	2 S33300	probable substance
24	18	26.9	12	2 S25056	Ig heavy chain - m
25	18	26.9	12	2 151678	gene rLPL-A protein
26	18	26.9	12	2 PH1459	T-cell receptor beta
27	17.5	26.1	8	2 JS0315	leucokinin V - Mad
28	17	25.4	7	2 PT0586	T-cell receptor beta
29	17	25.4	8	2 A44960	neuropeptide Led-C

ALIGNMENTS

RESULT 1

C39191 hypothetical protein 1 (retx' 5' region) - *Bacteroides fragilis*

C;Species: *Bacteroides fragilis*

C;Date: 08-Nov-1991 #sequence_revision 08-Nov-1991

C;Accession: C39191

R;Speer, B. S.; Bedzyk, L.; Salyers, A. A.

J. Bacteriol. 173, 176-183, 1991

A;Title: Evidence that a novel tetracycline resistance gene found on two *Bacteroides* tr:

A;Reference number: A39191; PMID:9100280; PMID:1846135

A;Accession: C39191

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-10 <SPB>

A;Cross-references: GB:M37699

Query Match Score 44.8%; Pred. No. 32;

Best Local Similarity 62.5%; Mismatches 5;

Matches 5; Conservative 1;

Indels 0; Gaps 0; Gaps 0;

Query Match Score 30; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 32;

Matches 5; Conservative 1;

Indels 0; Gaps 0; Gaps 0;

Query Match Score 28; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 2;

Indels 0; Gaps 0; Gaps 0;

Query Match Score 41.8%; Pred. No. 32;

Best Local Similarity 62.5%; Mismatches 9;

Matches 2 YFSRPPWTS 9;

Query Match Score 28; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 2;

Indels 0; Gaps 0; Gaps 0;

Query Match Score 41.8%; Pred. No. 32;

Best Local Similarity 62.5%; Mismatches 9;

Matches 2 YFSRPPWTS 9;

RESULT 2

S36850 Ig heavy chain V region - mouse

C;Species: *Mus musculus* (house mouse)

C;Accession: S36850

R;Jacob, J.; Kalsbeek, G.

submitted to the EMBL Data Library, July 1992

A;Description: In situ studies on the primary immune response to (4-hydroxy-3-nitrophenyl

A;Reference number: S25024

A;Accession: S36850

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-9 <JAC>

A;Cross-references: EMBL:X67387; NID:g50113; PID:CAA47799_1; PID:e51594; PID:91333871

C;Keywords: heterotetramer; immunoglobulin

Query Match Score 28; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 2;

Indels 0; Gaps 0; Gaps 0;

Query Match Score 41.8%; Pred. No. 32;

Best Local Similarity 62.5%; Mismatches 9;

Matches 2 YGSYF 6;

Db 4 DYGSYF 9;

RESULT 3

PT0274
 19 heavy chain CRD3 region (clone 3-109B) - human (fragment)
 C;Species: Homo sapiens (human)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0274
 R.;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J.;Exp. Med., 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
 A;Reference number: PMID:108337; MUID:9108337; PMID:1899102
 A;Accession: PT0274
 A;Molecule type: DNA
 A;Residues: 1-12 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match Score 25; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSLWTS 12
 Db 3 YSSSWI 9

RESULT 4
 PH1602
 19 H chain V-D-J region (wild-type clone 313) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: PH1602
 R.;Levinson, D.A.; Campos-Torres, J.; Ledermann, P.
 J.;Exp. Med., 178, 317-329, 1993
 A;Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A;Reference number: PMID:15880; MUID:93301609; PMID:8315387
 A;Accession: PH1602
 A;Molecule type: DNA
 A;Residues: 1-7 LEV
 A;Experimental source: bone marrow pre-B lymphocyte
 C;Keywords: immunoglobulin

Query Match Score 24; DB 2; Length 7;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 SELWT 11
 Db 3 SSIWT 7

RESULT 5
 G41946
 T-cell receptor gamma chain (2t.23) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Accession: G41946
 R.;Whetsell, M.; Mobley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
 Mol. Cell. Biol., 11, 5902-5909, 1991
 A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma g
 A;Reference number: A41946; MUID:92049316; PMID:1558619
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-9 <WHE>
 C;Keywords: T-cell receptor

Query Match Score 22; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
 Db 2 YGSYSS 7

RESULT 6
 B34835
 dnaA protein - *Pseudomonas aeruginosa* (fragment)
 C;Species: *Pseudomonas aeruginosa*
 C;Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 08-Oct-1999
 C;Accession: B34835
 R.;Yee, T.W.; Smith, D.W.
 Proc. Natl. Acad. Sci. U.S.A. 87, 1278-1282, 1990
 A;Title: *Pseudomonas* chromosomal replication origins: a bacterial class distinct from Escherichia coli
 A;Reference number: A34835; MUID:90160310; PMID:2106132
 A;Accession: B34835
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-6 <WHE>
 A;Cross-references: GB:M30125; NID:9151419; PIDN:AAA25916.1; PMID:9151421
 C;Keywords: DNA binding

Query Match Score 29.9%; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 BLW 10
 Db 4 BLW 6

RESULT 7
 T13838
 cytochrome-c oxidase (EC 1.9.3.1) chain I - *Bipes biporus* mitochondrion (fragment)
 C;Species: mitochondrion *Bipes biporus* (fragment)
 C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
 C;Accession: T13838
 R.;Macey, J.R.; Larson, A.; Ananjeva, N.B.; Pang, Z.; Papenfuss, T.J.
 Mol. Biol. Evol., 14, 91-104, 1997
 A;Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A;Reference number: Z17789; MUID:9715326; PMID:900757
 A;Accession: T13838
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-10 <AAC>
 A;Cross-references: UNIPROT:P922576; EMBL:U71335; NID:91753232; PIDN:AAAB482
 C;Genetics:
 A;Genome: mitochondrion
 A;Note: COI
 C;Keywords: mitochondrion; oxidoreductase

Query Match Score 29.9%; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFES 7
 Db 6 SFES 9

RESULT 8
 S05002
 corazonin - American cockroach
 C;Species: Periplaneta americana (American cockroach)
 C;Accession: S05002
 R.;Veenstra, J.A.
 FEBS Lett., 250, 231-234, 1989
 A;Title: Isolation and structure of corazonin, a cardioactive peptide from the american
 A;Reference number: S05002; MUID:8932572; PMID:2753132
 A;Accession: S05002
 A;Molecule type: protein
 A;Residues: 1-11 <WEE>
 A;Cross-references: UNIPROT:P11496
 C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid (Gln) #status experimental
 F;1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental
 F;1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match Score 20; DB 2; Length 11;
Best Local Similarity 42.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy :|: 6 FSBLWTS 12
Db 5 YSRGWTN 11

RESULT 9
B61445 Leu-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Accession: B61445
R;Leung, M.K.; Stefanoff, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A;Reference number: A61445; MUID:84144823; PMID:6583690
A;Accession: B61445
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match Score 19; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy :|: 2 YGSF 5
Db 1 YGGF 4

RESULT 10
A61445 Met-enkephalin - blue mussel
C;Species: Mytilus edulis (blue mussel)
C;Accession: B61445
R;Leung, M.K.; Stefanoff, G.B.
Proc. Natl. Acad. Sci. U.S.A. 81, 955-958, 1984
A;Title: Isolation and identification of enkephalins in pedal ganglia of Mytilus edulis
A;Reference number: A61445; MUID:84144823; PMID:6583690
A;Molecule type: protein
A;Residues: 1-5 <LEU>
A;Experimental source: pedal ganglia
C;Keywords: neuropeptide; opioid peptide

Query Match Score 19; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy :|: 2 YGSF 5
Db 1 YGGF 4

RESULT 11
PT0519 T-cell receptor beta chain V-D-J region (100-4C) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: PT0519
R;Feeney, A.J.
J. Exp. Med. 174, 115-124, 1991
A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
A;Reference number: PT0509; MUID:91277601; PMID:1711558
A;Accession: PT0519
A;Status: translation not shown
A;Molecule type: mRNA

A;Residues: 1-6 <PEE>
A;Experimental source: adult thymus, strain BALB/c
C;Keywords: T-cell receptor

Query Match Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 SELW 10
Db 2 SSILW 5

RESULT 12
A43129 neuropeptide GNFFRFamide - tapeworm (Moniezia expansa)
C;Species: Moniezia expansa
C;Date: 10-Nov-1997 #sequence_revision 14-Nov-1997 #text_change 09-Jul-2004
C;Accession: A43129
R;Maule, A.; Shaw, C.; Halton, D.; Thim, L.
Biochem. Biophys. Res. Commun. 193, 1054-1060, 1993
A;Title: GNFFRFamide: A novel FMRFamide-immunoreactive peptide isolated from the sheep t.
A;Reference number: A43129; MUID:93312289; PMID:8323531
A;Accession: A43129
A;Molecule type: protein
A;Cross-references: UNIPROT:P41966
A;Keywords: amidated carboxyl end; neuropeptide
F;6/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match Score 19; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy :|: 3 GSFF 6
Db 1 GNFF 4

RESULT 13
A60224 Met-enkephalin-Arg-Phe - rabbit
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 21-Oct-1992 #sequence_revision 21-Oct-1992 #text_change 02-Sep-2000
C;Accession: A60224
R;Madden IV, J.; Evans, C.J.; Tyler, A.N.; Esch, F.S.; Boehlen, P.; Nakk, G.; Weber, E.
J. Neurochem. 56, 1914-1920, 1991
A;Title: Isolation and characterisation of opioid peptides from rabbit cerebellum.
A;Reference number: A60224; MUID:91225580; PMID:2027006
A;Accession: A60224
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <MD>
C;Superfamily: proenkephalin
C;Keywords: neuropeptide; opioid peptide

Query Match Score 19; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy :|: 2 YGSF 5
Db 1 YGGF 4

RESULT 14
A41117 acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
C;Species: Naja naja oxiana (Asian cobra, Orixus cobra)
C;Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C;Accession: A41117
R;Kreienkamp, H.J.; Weise, C.; Raba, R.; Aaviksaar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:31:27 ; Search time 174 Seconds

(without alignments)
35.316 Million cell updates/sec

Title: US-10-088-681-2

Perfect score: 67
Sequence: 1 EYGSIFFSELWTS 12Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4233

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : UniProt_03;*
1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	24	35.8	11 2	077895 oreochromis
2	24	35.8	11 2	077895 oreochromis
3	23	34.3	11 2	077895 oreochromis
4	22	32.8	12 2	P83537 lactobacill
5	21	31.3	9	Q9TRT7 bos taurus
6	20	29.9	10 2	095953 homo sapien
7	20	29.9	10 2	Q61A62 homo sapien
8	20	29.9	11 1	P92576 bipes bipor
9	20	29.9	11 2	P11496 periplaneta
10	20	29.9	11 2	077894 oreochromis
11	20	29.9	11 2	077898 oreochromis
12	20	29.9	12 2	Q65CG7 sinaloa tom
13	20	29.9	12 2	Q46664 macropus ro
14	19	28.4	6 1	F4PZ PERAM
15	19	28.4	8 2	P41966 monilezia ex
16	19	28.4	8 2	Q99M00 mus musculu
17	19	28.4	10 2	Q7L227 naja oxiana
18	19	28.4	10 2	Q9TR47 bos taurus
19	19	28.4	11 2	Q8SHC6 furcifer be
20	19	28.4	12 2	Q9UC46 homo sapien
21	19	28.4	12 2	Q53579 rhodobacter
22	18	26.9	8 2	Q63579 ractus norv
23	18	26.9	8 2	Q68LF1 myrmotherul
24	18	26.9	9 1	Q68LG3 sakesphorus
25	18	26.9	9 2	P08946 phyllomedus
26	18	26.9	9 2	Q9H3Y3 homo sapien
27	18	26.9	9 2	Q8H9Z1 cyanophage
28	18	26.9	10 1	P03350 gb virus c/
29	18	26.9	10 2	Q81626 locusta mig
30	18	26.9	10 2	Q7M465 PHYRO
31	18	26.9	10 2	Q8SHB1 rhampholeura
				Q8SHB4 furcifer ve

ALIGNMENTS

RESULT 1									
ID	AC	DT	DT	DT	DT	DT	DT	DT	PRT;
077895	O77895	077895	077895	077895	077895	077895	077895	077895	PRELIMINARY;
		01-NOV-1998	(TREMBLrel.	08,	Created)				
		01-NOV-1998	(TREMBLrel.	08,	Last sequence update)				
		01-DEC-2001	(TREMBLrel.	19,	Last annotation update)				
					MHC class II B locus 12 (Fragment)				
					Oreochromis niloticus (Nile tilapia) (Tilapia nilotica)				
					Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Butteleoste; Neoteleoste;				
					Acanthomorpha; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Oreochromis.				
					NCBI_TaxID=8128;				
					RN [1]				
					SEQUENCE FROM N.A.				
					MEDLINE=9815113; PubMed=9649539;				
					RX				
					Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,				
					Figuerola F., Sultmann H., Klein J./				
					"Linkage relationships and haplotype polymorphism among cichlid MHC class II B loci";				
					Genetics 149:1527-1537(1998).				
					EMBL; AF050005; AAC134.1; -.				
					NON_TER 1				
					SEQUENCE 11 AA; 1367 MW;				
					3P4TC9EA772045A3 CRC64;				
					RL				
					FT				
					NON_TER 1				
					SEQUENCE 11 AA; 1367 MW;				
					3P4TC9EA772045A3 CRC64;				
					Query Match 35.8%;				
					Best Local Similarity 50.0%;				
					Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;				
					Qy 5 FFSELMNTS 12				
					Db 3 FWSILWVA 10				
					RN [1]				
					SEQUENCE FROM N.A.				
					MEDLINE=9815113; PubMed=9649539;				
					RX				
					Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,				

RA Figueiro P.; Sultmann H.; Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 RT class II loci.";
 RL Genetics 149:1527-1537(1998).
 EMBL AF050006; AAC1345..1.; -.
 FT NON-TER 1 1
 FT NON-TER 11 11
 SEQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;
 Query Match Similarity 35.8%; Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 FFSELW 10
 Db 3 FWSMLW 8

RESULT 3
 P83537 PRELIMINARY; PRT; 11 AA.
 ID P83537; PRELIMINARY; PRT; 11 AA.
 AC P83537; PRELIMINARY; PRT; 11 AA.
 DR 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 NCBITaxID=1625;
 RN [1] ANNE, AND INDUCTION.
 RC STRAIN DSM 20451;
 RP Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RA Lulli L.; Torchiana B.; Pinocchiaro G.;
 DR Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR U77631; AAD15626..1.; -.
 DR GO:0004336; P:galactosylceramidase activity; IEA.
 DR GO:0016798; P:hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; P:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON-TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2ADD2C99C8 CRC64;
 CC -!- INDUCTION: By elevated hydrostatic pressure.
 CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 CC protein is: 65 kDa.
 FT NON-TER 1 1
 FT NON-TER 11 11
 SEQ SEQUENCE 11 AA; 1249 MW; D96C8231B771ADD9 CRC64;
 Query Match Similarity 34.3%; Score 23; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GSFFFS 7
 Db 1 GSFFFA 5

RESULT 4
 Q9TRT7 PRELIMINARY; PRT; 12 AA.
 ID Q9TRT7; PRELIMINARY; PRT; 12 AA.
 AC Q9TRT7; PRELIMINARY; PRT; 12 AA.
 DR 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE 15 kDa amyloid protein A homolog (Fragment).
 OS Bos taurus (Bovine).
 OC Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae;
 Bovine; Bos
 OC Sequences; Bos
 NCBITaxID=9913;
 RN [1] Veiby O.P.; Sletten K.; Husby G.; Nordstoga K.;
 RX MEDLINE=92132498; PubMed=1734497;
 RA "Amino acid sequence analyses of non-AA proteins from amyloid fibrils
 RT

RA Figuerio P.; Sultmann H.; Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 RT class II loci.";
 RL Genetics 149:1527-1537(1998).
 EMBL AF050006; AAC1345..1.; -.
 FT NON-TER 1 1
 SEQ SEQUENCE 11 AA; 1399 MW; 3F47DB7A772685A3 CRC64;

Query Match Similarity 35.8%; Score 24; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 4 SFSELW 10
 Db 1 SFFXEY 7

RESULT 5
 ID 095953 PRELIMINARY; PRT; 9 AA.

AC 095953; PRELIMINARY; PRT; 9 AA.
 DR 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DR Galactocerobrosidase (EC 3.2.1.46) (Fragment).
 GN Name=GALC;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] TISSUE=Brain;
 RC SEQUENCE FROM N.A.
 RA Lulli L.; Torchiana B.; Pinocchiaro G.;
 DR Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR U77631; AAD15626..1.; -.
 DR GO:0004336; P:galactosylceramidase activity; IEA.
 DR GO:0016798; P:hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO:0005975; P:carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON-TER 9
 SQ SEQUENCE 9 AA; 1069 MW; 374E2ADD2C99C8 CRC64;

Query Match Similarity 31.3%; Score 21; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 1.6e+06;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 GSFFFS 7
 Db 2 GFNVAIDLW 9

RESULT 6
 Q6LA62 PRELIMINARY; PRT; 10 AA.

AC Q6LA62; PRELIMINARY; PRT; 10 AA.
 DR 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Amiloride-sensitive epithelial sodium channel gamma subunit
 DE (Fragment).
 GN Name=SCNN1G;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=96121598; PubMed=8824247; DOI=10.1074/jbc.271.42.26062;
 RX Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;
 RA "Genomic organization and the 5' flanking region of the gamma subunit
 RT of the human amiloride-sensitive epithelial sodium channel.";
 RL J. Biol. Chem. 271:26062-26065(1996).
 RN [2] SEQUENCE FROM N.A.
 RP

MEDLINE=98316780; PubMed=9654208;
 RX Marynen P., Bidlingmaier F.;
 RA Ludwig M., Bolkenius U., Wickert L.,
 RT "structural organization of the gene encoding the alpha-subunit of the
 human amiloride-sensitive epithelial sodium channel.";
 RL Genet. 102:576-581(1998).
 EMBL; CABN;
 DR CAH07506.1; -;
 GO: GO:00052216; F:ion channel activity; IEA.
 KW Ionic channel.
 PT NON-TER 1 1
 FT 10 10
 SQ SEQUENCE 10 AA; 1157 MW; DBAFF8133733B05A2 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 4 SFPSFLW 10
 Db 1 SVVSEKW 7

RESULT 7
 P92576 PRELIMINARY; PRT; 10 AA.
 AC 092576;
 DT 01-MAY-1997 (TRIMBLrel. 03; Created)
 DT 01-MAY-1997 (TRIMBLrel. 03; Last sequence update)
 DT 01-OCT-2003 (TRIMBLrel. 25; Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Name=C01;
 OS Biporus biporus (Baja worm lizard).
 OG Mitochondrion.
 OC Lepidosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Squamata; Scleroglossa; Amphisbaenia; Bipedidae; Bipes.
 OC NCBITAXID=52188;
 RN [1]

SEQUENCE FROM N.A.
 MEDLINE=97153826; PubMed=9000757;
 RX Macey J.R., Larson A., Ananjeva N.B., Fang Z., Papenfuss T.J.;
 RA "Two novel gene orders and the role of light-strand replication in
 rearrangement of the vertebrate mitochondrial genome.";
 RT Mol. Biol. Evol. 14:91-104(1997).
 RN [2]
 SEQUENCE FROM N.A.
 MEDLINE=97153820; PubMed=9000751;
 RX Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
 RT "Replication slippage may cause parallel evolution in the secondary
 structures of mitochondrial transfer RNAs.";
 RL Mol. Biol. Evol. 14:30-39(1997).
 EMBL; U71335; AAB48271.1;
 PIR; T13838; TI3838.
 KW Mitochondrion.
 PT NON-TER 10 10
 SQ SEQUENCE 10 AA; 1176 MW; SB3580C9D5A411A7 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFPS 7
 Db 6 SFPS 9

RESULT 8
 CORZ PERAM STANDARD; PRT; 11 AA.
 ID CORZ_PERAM
 AC P114956;
 DT 01-OCT-1989 (Rel. 12; Created)
 DT 01-FEB-1994 (Rel. 28; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DE Corazonin.

OS Periplaneta americana (American cockroach).
 OC Neoptera; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Blattidae; Orthopteroidea; Dictyoptera; Blattoidea.
 OX NCBITAXID=6978;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cordata Cardiaca;
 RX MEDLINE=89325572; PubMed=101016/0014-5793(89)80727-6;
 RX MEDLINE=89325572; PubMed=2753132; DOI=10.1016/0014-5793(89)80727-6;
 SQ Sequence from the
 RA Veensira J.A.;
 RT "Isolation and structure of corazonin, a cardioactive peptide from the
 American cockroach,"
 RL FEBS Lett. 250:231-234 (1989).
 CC -I- FUNCTION: Cardioactive peptide. Corazonin is probably involved in
 the physiological regulation of the heart beat.
 CC -I- SUBCELLULAR LOCATION: Secreted.
 DR PIR; S05002; S05002.
 KW Amidation; Direct protein sequencing; Neuropeptide;
 KW Pyrrolidone carboxylic acid.
 PT MOD-RES 1 1 Pyrrolidone carboxylic acid.
 PT MOD-RES 11 11 Asparagine amide.
 SQ SEQUENCE 11 AA; 1387 MW; C7CF52D6415AB46 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 11;
 Best Local Similarity 42.9%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FSBLWTS 12
 Db 5 YSRGWTN 11

RESULT 9
 P077894 PRELIMINARY; PRT; 11 AA.
 AC 077894;
 DT 077894;
 DR 077894;
 SEQUENCE FROM N.A.
 MEDLINE=98315113; PubMed=9649539;
 RX Malaga-Trillo F., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figuerola P., Sultmann H., Klein J.;
 DT 01-NOV-1998 (TRIMBLrel. 08; Last sequence update)
 DT 01-NOV-1998 (TRIMBLrel. 08; Last annotation update)
 DB MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidei;
 OC Cichlidae; Oreochromis.
 RN [1]
 SEQUENCE FROM N.A.
 MEDLINE=98315113; PubMed=9649539;
 RX Malaga-Trillo F., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 RA Figuerola P., Sultmann H., Klein J.;
 DT 01-DEC-2001 (TRIMBLrel. 19; Last annotation update)
 DB Class II B loci;"
 RT Linkage relationships and haplotype polymorphism among cichlid MHC
 RL Genetics 149:1527-1537(1998).
 DR EMBL; AF050004; AAC41343.1; -.

Query Match 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 FFSELW 10
 Db 3 FWSIVW 8

RESULT 10
 ID 077898
 ID 077898 PRELIMINARY; PRT; 11 AA.
 AC 077898;
 AC 077898;
 DT 01-NOV-1998 (TRIMBLrel. 08; Created)

01-NOV-1998 (TrEMBLrel. 08; Last sequence update)
 DT DT-DEC-2001 (TrEMBLrel. 19; Last annotation update)
 MHC class II B locus 12 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Buteostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidei;
 Cichlidae; Oreoichromis.
 NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=9649539;
 RX MEDLINE=98315113;
 RA Malaga-Trillo B.; Zaleska-Rutczynska Z.; McAndrew B.; Vincsek V.;
 RA Figueras F.; Sulzmann H.; Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid MHC
 class II B loci.",
 RL Genetics 149:1527-1537(1999).
 DR EMBL; AF050008; AAC41347.1; -.
 FT NON-TER 1 1
 FT NON-TER 11 11
 SQ SEQUENCE 11 AA; 1367 MW; 3F47DC0A62C045A3 CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 RESULT 11
 Qy 5 FPFSEW 10
 Db 3 FWSIVW 8
 PRT; 11 AA.
 PRELIMINARY;
 ID Q65CG7
 AC Q65CG7;
 DT 25-OCT-2004 (TrEMBLrel. 28; Created)
 DT 25-OCT-2004 (TrEMBLrel. 28; Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28; Last annotation update)
 DE Transcriptional activator (Fragment).
 GN Name=AC22;
 OS Tomato leaf curl virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=71186
 RN RP
 SEQUENCE FROM N.A.
 RC Rojas A., Kvarnheiden A., Rodriguez D., Valkonen J.P.T.
 RT "A mixture of begomoviruses in severe leaf curl-affected tomatoes in
 Nicaragua."
 RT Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.
 DR AJ508781; CAD4523.1; -.
 FT NON-TER 1 1
 SQ SEQUENCE 11 AA; 1356 MW; 861BC90602D379DS CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04; Indels 0; Gaps 0;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 RESULT 12
 Qy 4 SFPSELMT 11
 Db 4 SFWVELF 11
 PRT; 12 AA.
 PRELIMINARY;
 ID Q46664
 AC Q46664;
 DT 01-JUN-1998 (TrEMBLrel. 06; Created)
 DT 01-JUN-1998 (TrEMBLrel. 06; Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19; Last annotation update)
 DE Glucosidase-6-phosphate dehydrogenase (Fragment).
 GN Name=GPD;
 OS Macropus robustus.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
 NCBI_TaxID=35589;
 RN [1]
 RP SEQUENCE FROM N.A.; PubMed=9060417;
 RX MEDLINE=9724585;
 RA Lobeel D.A.; Johnston P.G.;
 RT "Analysis of the intron-exon structure of the G6PD gene of the
 wallaroo (Macropus robustus) by polymerase chain reaction.";
 RL Mamm. Genome 8:146-147(1997).
 DR EMBL; U53774; AAC48789.1; -.
 FT NON-TER 1 1
 SQ SEQUENCE 12 AA; 1430 MW; D42A9C84E3CB1AA9 CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 GSFFES 8
 Db 2 GYFDE 7
 PRT; 12 AA.
 PRELIMINARY;
 ID Q61331
 AC Q61331;
 DT 01-NOV-1996 (TrEMBLrel. 01; Created)
 DT 01-MAY-1999 (TrEMBLrel. 10; Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update)
 DE N-acetylglucosamine beta1-4 galactosyl transferase (EC 2.4.1.90)
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 OX NCBI_TaxID=10309;
 RN RP
 SEQUENCE FROM N.A.; PubMed=89033997;
 RX Nakazawa K., Ando T., Kamura T., Narimatsu H.;
 RA RT "Cloning and sequencing of a full-length cDNA of mouse N-
 acetylglucosamine beta-1,4-galactosyltransferase.",
 RT acetylglucosamine (bet-1-4)galactosyltransferase.
 RL J. Biochem. 104:165-168(1988).
 DR EMBL; D00315; BAA00217.1; -.
 DR GO; GO:0003945; P:N-acetyl-lactosamine synthase activity; IBA,
 GO; GO:0016757; P:transferase activity, transferring glycosyl. . . ; IBA.
 KW Glycosyltransferase; Transferase.
 FT NON-TER 1 1
 SQ SEQUENCE 12 AA; 1283 MW; 304EA40668387728 CRC64;
 Query Match Similarity 29.9%; Score 20; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 1.5e+04; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 WTS 12
 Db 1 WTS 3
 PRT; 6 AA.
 PRELIMINARY;
 ID FAPR_MONEK
 AC FAPR_MONEK
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 05-JUL-2004 (Rel. 44; Last annotation update)
 DB FMRFamide-like neuropeptide GNFRP-amide.
 OS Monierhelia expansa (Sheep tapeworm)
 OC Eukaryota; Metazoa; Playyhelminthes; Cestoda; Eucestoda;
 OC Cyclopolyidae; Anoplocephalidae; Moniezia.
 NCBI_TaxID=2841;

```

RN [1]
RP SEQUENCE.
RX MEDLINE=93312289; PubMed=8323531;
RA Maule A.G.; Shaw C.; Halton D.W.; Thim L.;  

RT "GNFFRamide: a novel FMRFamide-immunoreactive peptide isolated from  

the sheep tapeworm, Moniezia expansa.";  

RL Biochim. Biophys. Res. Commun. 193:1054-1060(1993).
CC -!- SUBCELLULAR LOCATION: Secreted
CC -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC Family.
CC PIR: A43129; A41129.
KW Amidation; Direct protein sequencing; Neuropeptide.
MOD RES 6 Phenylalanine amide.
FT 6 AA; 787 MW; 69D409C9c481000 CRC64;
SQ SEQUENCE 6 AA; 787 MW; 69D409C9c481000 CRC64;

Query Match 28.4%; Score 19; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 3 GSFP 6
          :|:
Db 1 GNFF 4

RESULT 15
Q99MNO
ID Q99MNO PRELIMINARY;
PRT; 8 AA.
AC Q99MNO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Adenosine deaminase tRNA-specific 1 (Fragment).
GN Name=adat1;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
NCBI TaxID=10096;
RN [1]
RP SEQUENCE FROM N.A.
STRAIN=129/SvJ;
RX MEDLINE=21231131; PubMed=11331948;
RA Maas S.; Kim Y.G.; Rich A. ;
RT "Genomic clustering of tRNA-specific adenosine deaminase ADAT1 and two  

tRNA synthetases.";
RL Mamm. Genome 12:387-393 (2001).
DR EMBL; AF328904; AK19310.1; .
DR MGD; MGI:13533631; Addt1.
FT NON-TER 8 8
SQ SEQUENCE 8 AA; 936 MW; F4D05B1AADC1B376 CRC64;

Query Match 28.4%; Score 19; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 9 IWTs 12
          :|:
Db 1 MWTs 4

Search completed: April 27, 2005, 15:46:23
Job time : 176 secs

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OM protein - protein search, using sw model

Run on: April 27, 2005, 15:39:49 ; Search time 167 Seconds (without alignments)

Total number of hits satisfying chosen parameters: 520583

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqp1980B:
3: geneseqp2000B:
4: geneseqp2001B:
5: geneseqp2002B:
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7: geneseqp2003Bs:
8: geneseqp2004B:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULTS

	RESULT 1	
ID	AAB86005	standard; peptide; 12 AA.
XX		
AC	AAB86005;	
XX		
DT	12-JUL-2001	(first entry)
XX		
DB	DCM-associated peptide #5.	
XX		
KW	DCM; dilatative cardiomyopathy; autoantibody; cardiant;	
XX		
KW	beta-1 adrenergic activated antibody; immuno-suppressive.	
OS	Synthetic.	
XX		
PN	WO200121660-A1.	
XX		
PD	29-MAR-2001.	
XX		
PP	21-SEP-2000; 2000WO-EP009241.	
XX		
PR	21-SEP-1999; 99EP-00118630.	
XX		
PR	21-SEP-1999; 99EP-00118631.	
XX		
PA	(AIFI-) APPINA IMMUNTECHNIK GMBH.	
XX		
PI	Roenspeck W, Kunze R, Wallukat G, Dierenthal M;	
XX		
DR	WPI; 2001-335469/35.	
XX		
PT	New peptide useful for combating the autoantibodies that are responsible for dilatative cardiomyopathy.	
PT		
PS	Claim 3: Page 20: 29pp; German.	
XX		

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	82.1	12	4 AAB86005	Aab86005 DCM-associated
2	34	50.7	6	5 AAM47222	Aab97294 Beta1-adr
3	34	50.7	6	5 ADP49242	Aam47222 Dilated c
4	34	50.7	6	3 AAB09130	Disease-a
5	34	50.7	8	3 AAB09130	Aab9130 Hepatitis
6	31	46.3	10	8 ADK09671	Adk09671 Human pap
7	31	46.3	10	8 ADR09188	Adk09188 Human pap
8	30	44.8	6	6 ABR46515	Abr46515 Staphyloc
9	30	44.8	9	2 AAW72493	Aaw72493 Dengue vi
10	30	44.8	10	2 AAW76040	Aaw76040 Lm609 Gra
11	30	44.8	10	2 AAW37198	Aaw37198 Human onc
12	30	44.8	10	4 AAB61398	Aab61398 Multiple
13	30	44.8	10	6 ABO19836	Abo19836 Enhanced
14	30	44.8	10	7 ADG71874	Enhanced
15	30	44.8	10	8 ADG5055	Adg71874 Enhanced
16	29	43.3	7	3 AAY33139	Adg5055 Murine LM
17	29	43.3	10	5 AAU93215	Aay33139 Rabbit ca
18	29	43.3	11	6 AB37125	Aau93215 Granulocy
19	29	43.3	12	4 AAM00568	Abj37125 Rhodopain
20	28	41.8	6	6 ABR46459	Aam00568 Human str
21	28	41.8	7	8 ADR68302	Abr46459 Staphyloc
22	28	41.8	8	8 ADK09492	Adr68302 Androgen
23	28	41.8	9	8 AAO4678	Adk09492 Human pap
24	28	41.8	9	8 ADK09532	Aao4678 Peptide #
25	28	41.8	9	8 ADK09531	Adk09532 Human pap
				Sequence 12 AA;	
				Query Match	82.1% ; Score 55 ; DB 4 ; Length 12 ;
				Best Local Similarity	100.0% ; Pred. No. 0.013 ;

XX AC ADP49242;
 XX DT 09-SEP-2004 (First entry)
 XX Disease-associated autoantibody detection method peptide #1.
 XX KW cardiant; gynaecological; immunosuppressive; hypotensive; antipsoriatric;
 XX KW vasotropic; disease-associated autoantibody; antibody;
 XX G protein-coupled receptor.
 XX Unidentified.
 OS
 PN WO2004051280-A2.
 XX PD 17-JUN-2004.
 XX PF 28-NOV-2003; 2003WO-DE003988.
 XX PR 29-NOV-2002; 2002DE-01056897.
 XX PR 27-JAN-2003; 2003DE-01003120.
 PR 13-JUN-2003; 2003DE-01027066.
 XX PA (DELB-) DELBRUECK CENT MOLEKULARE MEDIZIN MAX.
 XX PI Wallukat G;
 XX DR WPI: 2004-450802/42.
 XX PT Detecting disease-associated autoantibodies against G protein-coupled
 PT receptors, useful for diagnosing e.g. cardiomyopathy, comprises an
 PT enzymatic or color reaction.
 XX PS Claim 12; Page 49; 57PP; German.
 XX The present invention relates to a method for detecting disease-
 CC associated autoantibodies (AAb) directed against G protein-coupled
 CC receptors. This comprises treating a body fluid with a denaturing agent,
 CC treating the precipitate formed with a biotin-containing peptide having
 the (partial) sequence of a first and/or second loop of a G protein-
 CC coupled receptor, incubating the mixture with a carrier coated by
 CC (strept)avidin, washing the carrier and incubating it with labeled anti-
 CC immunoglobulin G (IgG) antibody subclases, and performing an enzymatic
 CC or colour reaction. The method is used to detect AAb associated with
 CC dilatative or Chagas cardiomyopathy, myocarditis, pre-eclampsia, humoral
 CC kidney rejection, malignant, essential, refractory or pulmonary
 CC hypertension, psoriasis and Raynaud's syndrome. The present invention is
 CC a peptide which can be used in the method of the invention.
 XX SQ Sequence 6 AA;
 Query Match 50.7%; Score 34; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX SQ 1 EYGSFF 6
 1 |||||
 Db 1 EYGSFF 6
 RESULT 5
 AAB09130 ID AAB09130 Standard; protein; 8 AA.
 XX AC AAB09130;
 XX DT 06-AUG-2003 (revised)
 DT 30-AUG-2000 (First entry)
 XX DB Hepatitis GB virus protein sequence SEQ ID NO:252.
 XX Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
 KW detection; characterisation; hepatitis.

XX OS Hepatitis GB virus.
 XX PN US6051374-A.
 XX PR 18-APR-2000.
 XX PD 07-JUN-1995; 95US-00438445.
 XX PR 14-FEB-1994; 94US-00196030.
 XX PR 13-MAY-1994; 94US-0024654.
 XX PR 29-JUL-1994; 94US-0028314.
 XX PR 23-NOV-1994; 94US-0034185.
 XX PR 23-NOV-1994; 94US-00344190.
 PR 30-JAN-1995; 95US-0037557.
 XX PA (ABB) Abbott LAB.
 XX PI Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buijik SL;
 PI Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;
 XX DR WPI: 2000-338307/29.
 XX PT Detecting target hepatitis GB virus nucleic acid in a test sample the HGBV
 PT suspected of containing HGBV comprises reacting the test sample the HGBV
 PT polynucleotide probe and detecting the complex that contains target HGBV.
 XX PS Example 9; Col 331-332; 369PP; English.
 XX CC The present invention describe a method for detecting target hepatitis GB
 CC virus (HGBV) nucleic acid (THN) in a test sample (T) with suspected of
 CC containing HGBV. The method involves reacting (T) with a HGBV
 CC polynucleotide probe (P) containing 15 contiguous nucleotides, and which
 CC selectively hybridizes to the HGBV genome or its full complement, and
 CC detecting the complex that contains THN indicating the presence of
 CC target HGBV. The method is used for detecting target HGBV nucleic acid in
 CC the test sample suspected of containing HGBV and for characterisation of
 CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non
 CC -B hepatitis causing agents collectively termed as hepatitis GB virus.
 CC AAA55270 to AA55489 and AAB0985 to AAB09480 represent nucleotide and
 CC protein sequences used in the exemplification of the present invention.
 CC (Updated on 06-AUG-2003 to correct OS Field.)
 XX SQ Sequence 8 AA;
 Query Match 50.7%; Score 34; DB 3; Length 8;
 Best Local Similarity 85.7%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 XX SQ 6 FSELNNTS 12
 6 |||||
 Db 1 FSHLWTS 7
 RESULT 6
 ADK09671 ID ADK09671 standard; peptide; 10 AA.
 XX AC ADK09671;
 XX DT 06-MAY-2004 (First entry)
 DB Human papillomavirus peptide #1726.
 XX KW pathogenic virus; alternative reading frame; antigenic determinant;
 KW viricide; vaccine; therapeutic agent; infection; HPV.
 OS Human papillomavirus.
 XX PN WO2004011550-A2.
 XX PD 05-FEB-2004.

PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 (INTE-) INTERCELL AG.
 Mattner F, Schmidt W, Habel A;
 XX
 DR; 2004-169243/16.
 PT New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
 XX
 PT New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.
 XX
 PS Claim 18; Page 187; 220pp; English.
 XX
 CC This invention relates to a novel polypeptide encoded by an alternative reading frame of a pathogenic virus, where the polypeptide starts with a methionine amino acid residue, which comprises an antigenic determinant and more than 7 amino acid residues. The invention may be useful for the production of compounds with a virucide activity or the development of a vaccine. The polypeptide or its fragments may be useful as a therapeutic agent. It is also useful for the manufacture of a medicament for treating or preventing an infection with the pathogenic virus. The present sequence is that of a human papillomavirus (HPV) epitope peptide of the invention.
 XX
 Sequence 10 AA;
 SQ Query Match Score 31; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 SFPSRLNT 11
 Db 1 SFPSRLWS 8

RESULT 8
 ABR46515 standard; peptide: 6 AA.
 TD ABR46515 standard; peptide: 6 AA.
 XX
 AC ABR46515;
 XX DT 10-JUN-2003 (First entry)
 DE Staphylococcus aureus CHIPS-related peptide #1705.
 XX
 KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; CSaR;
 KW Formylated Peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KW inflammation; cardiovascular disease; central nervous system disease;
 KW gastrointestinal disease; skin disease; genitourinary disease;
 KW joint disease; respiratory disease; HIV infection; antinflammatory;
 KW cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KW synecological; immunosuppressive; anti-HIV.
 XX
 OS Synthetic.
 XX
 PN WO2003006048-A1.
 XX
 PD 23-JUN-2003.
 XX
 PR 11-JUL-2001; 2001WO-EP008004.
 XX
 PA (JARI-) JARI PHARM BV.
 XX
 PI Van Kessel CPM, Gosselaar-De Haas CJC, Kruijtzer JAW;
 PI Van Strijp JAG;
 XX
 DR; 2003-256333/25.
 XX
 Combination of peptides derived from chemotaxis inhibiting protein from Staphylococcus aureus (CHIPS) having CHIPS activity, useful in prophylaxis and treatment of inflammation, cardiovascular, skin and kidney diseases.
 XX
 Disclosure; Page 17; 89pp; English.

PS The present invention relates to peptides (ABR44811-ABR47162 and ABR47164 -ABR47385) derived from the Chemotaxis Inhibitory Protein (CHIPS) from Staphylococcus aureus. The peptide fragments are useful in the prophylaxis or treatment of diseases or disorders involving the C5a-receptor (C5aR) and/or Formylated Peptide receptor (FPR) or neutrophils, monocytes and endothelial cells or involving acute or chronic

PF 24-JUL-2003; 2003WO-EP008112.
 XX
 Human papillomavirus peptide #1243.
 XX
 Pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.
 XX
 Human Papillomavirus.
 OS WO2004011650-A2.
 PN 05-FEB-2004.
 PD 06-MAY-2004 (first entry)
 XX
 DE Human papillomavirus peptide #1243.
 XX
 KW Pathogenic virus; alternative reading frame; antigenic determinant; virucide; vaccine; therapeutic agent; infection; HPV.
 XX
 OS Human Papillomavirus.
 PN WO2004011650-A2.
 PD 05-FEB-2004.
 XX
 PP 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTE-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX
 DR; 2004-169243/16.
 PT New polypeptide encoded by an alternative reading frame of a pathogenic virus comprising an antigenic determinant, useful for treating or preventing an infection with the pathogenic virus.

CC inflammation reactions. The diseases or disorders include cardiovascular
 CC diseases, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 XX respiratory diseases and Hiv infection

Sequence 6 AA;

Query Match 44.8%; Score 30; DB 6; Length 6;
 Best Local Similarity 83.3%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 5 PPPBLW 10
 | | |
 Db 1 FPPBLW 6

RESULT 9

AAW72493 standard; peptide: 9 AA.
 ID AAW72493
 XX AC
 XX DT 23-DEC-1998 (first entry)
 XX DB Dengue virus type-2 glycoprotein NS1 peptide for epitope mapping #38.
 XX KW Dengue virus type-2 glycoprotein NS1; dengue haemorrhagic fever; DHF;
 KW dengue shock syndrome; DSS; Aedes aegypti; mosquito; antigen; vaccine;
 KW immunisation; immunoreactive; infection.
 OS Dengue virus.

US5824506-A.
 XX PN
 XX PD 20-OCT-1998.
 XX PP 15-AUG-1994; 94US-00290268.
 XX PR 15-AUG-1994; 94US-00290268.

PA (GENE-) GENELABS DIAGNOSTICS PTE LTD.

XX PI Chan L, Guan M;
 XX DR WPI: 1998-582552/49.
 XX PT Dengue virus peptide antigens - especially for diagnosis of dengue virus
 infection.
 XX Example 1; Col 17; 21pp; English.
 XX AAW72493 to AAW72570 represent peptide fragments from the dengue virus
 CC type-2 glycoprotein NS1, which was used in an example from the present
 CC invention for an epitope mapping assay. The invention has developed
 CC peptide antigens consisting of fragments of the dengue virus NS1 protein.
 CC The peptide antigens can be used for the diagnosis of dengue virus
 CC infection by detection of antibodies to the virus, especially in an assay
 CC comprising attaching the antigen to a solid support, contacting a serum
 CC sample with the support, and detecting bound antibodies with a labelled
 CC anti-human antibody or used for preparing vaccines against dengue virus
 XX

Sequence 9 AA;

Query Match 44.8%; Score 30; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;
 Matches 3 GSPPSELM 10
 | : | : |
 Db 1 GVFFPTNWW 8

RESULT 10
 AAW76040 standard; peptide: 10 AA.
 ID AAW76040;
 XX AC
 XX DT 02-NOV-1998 (first entry)
 XX DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
 XX KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; v-H region; CDR;
 KW complementarity determining region.
 XX OS Mus sp.
 XX PN WO9833919-A2.
 XX PD 06-AUG-1998.
 XX PF 30-JAN-1998; 98WO-US001826.
 XX PR 30-JAN-1997; 97US-00791391.
 XX PA (IXSY-) IXSYS INC.
 XX PI Huse WD, Glaser SM;
 XX DR WPI: 1998-437472/37.
 XX DR N-PSDB; AAV49877.
 XX PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis.
 XX PS Claim 62; Page 43; 129pp; English.
 XX CC AAW76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block integrin-
 CC mediated signal transduction. This is useful in the treatment, prevention
 CC and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis
 CC and restenosis (but also e.g. (non-)immune inflammation, diabetic
 CC retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 XX CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody
 XX SQ Sequence 10 AA;

Query Match 44.8%; Score 30; DB 2; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 SQ 2 YGSFIS 7
 5 YGSFIS 10

RESULT 11
 AAW37198 standard; peptide: 10 AA.
 ID AAW37198;
 XX AC
 XX DT 20-JUL-1998 (first entry)
 XX

PR 30-JAN-1998; 98US-00016061.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 Huse WD;
 PI
 PT WPI; 2003-492042/46.
 XX
 DR N-PSDB; ACD30195.
 XX
 PT LM609 grafted antibody exhibiting selective binding affinity to alphavbeta3 useful for treating an alphavbeta3-mediated disease e.g., angiogenesis or restenosis.
 XX
 PS Clam 62; Page 13; 71pp; English.
 XX
 CC The invention relates to a Vitaxin or LM609 grafted antibody exhibiting selective binding affinity to alpha_vbeta_3. The Vitaxin or LM609 grafted antibody is useful for treating an alpha_vbeta_3-mediated disease e.g., angiogenesis or restenosis. The present sequence represents the amino acid sequence of a LM609 complementarity determining region
 XX Sequence 10 AA;
 SQ Query Match Score 30; DB 6; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 YGSFFS 7
 ||||:
 Db 5 YGSFYS 10

RESULT 14
 ADG71874 standard; protein; 10 AA.
 XX
 AC ADG71874;
 XX DT 11-MAR-2004 (first entry)
 DE Enhanced LM609 grafted antibody VH region CDR3 #15.
 XX
 KW Grafted antibody; high affinity; alphavbeta3; inflammatory disorder; complementarity determining region; CDR; inflammation; immune inflammation; non-immune inflammation;
 KW chronic articular rheumatism; psoriasis; vessel disorder;
 KW diabetic retinopathy; neovascular glaucoma; capillary proliferation;
 KW atherosclerotic plaque; cancer disorder; antiinflammatory; antirheumatic;
 KW dermatological; immunosuppressive; ophthalmological; humanised;
 OS Synthetic.
 OS Homo sapiens.
 XX US6596850-B1.
 PN
 PD 22-JUL-2003.
 XX PP 30-JAN-1998; 98US-00016061.
 XX PR 30-JAN-1998; 98US-00016061.
 PA (IXSY-) IXSYS INC.
 XX
 PI Huse WD;
 XX DR WPI; 2004-081749/08.
 XX
 PR New Vitaxin antibody and a LM609 grafted antibody exhibiting selective binding affinity to alphavbeta3, useful for treating alphavbeta3-mediated diseases, e.g., angiogenesis and restenosis. The present sequence is murine LM609
 PT antibody variable region CDR mutant peptide.
 XX
 PS Claim 6; SEQ ID NO 100; 66pp; English.

XX
 CC The present invention relates to a high affinity LM609 grafted antibody exhibiting selective binding to alphavbeta3, or its functional fragment comprising one or more complementarity determining regions (CDRs) having at least one amino acid substitution in one or more CDRs of the LM609 grafted heavy chain variable region of a polypeptide having 117 amino acids or a grafted light chain variable region polypeptide having 107 amino acids. Also disclosed are polynucleotide sequences encoding the novel antibody or its functional fragment, and a composition comprising the novel antibody or its functional fragment. The antibodies and their fragments are useful for treating alphavbeta3-mediated diseases, e.g., inflammatory disorders such as immune and non-immune inflammation, chronic articular rheumatism, psoriasis, disorders associated with inappropriate or inappropriate invasion of vessels such as diabetic retinopathy, neovascular glaucoma, and capillary proliferation in atherosclerotic plaques as well as cancer disorders. The present sequence represents an antibody region.
 XX
 SQ Sequence 10 AA;
 SQ Query Match Score 30; DB 7; Length 10;
 Best Local Similarity 83.3%; Pred. No. 2.2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 RESULT 15
 ADJ58055 standard; peptide; 10 AA.
 XX
 AC ADJ58055;
 XX DT 06-MAY-2004 (first entry)
 DE Murine LM609 heavy chain variable region (VH) CDR3 mutant peptide #15.
 XX
 KW Vitaxin; antibody; LM609; angiogenesis; restenosis; therapy;
 KW variable region; mouse; mutant; mutein.
 XX
 OS Synthetic.
 XX
 PN US2004006213-A1.
 XX
 PD 08-JAN-2004.
 XX PP 16-JUN-2003; 2003US-00463847.
 XX
 PR 30-JAN-1997; 97US-00711391.
 XX PR 30-JUN-1998; 98US-00016061.
 XX
 PA (IXSY-) IXSYS INC.
 XX
 PI Huse WD, Glaser SM;
 XX DR WPI; 2004-081749/08.
 XX
 PR New Vitaxin antibody and a LM609 grafted antibody exhibiting selective binding affinity to alphavbeta3, useful for treating alphavbeta3-mediated diseases, e.g., angiogenesis or restenosis.
 XX
 PS Claim 62; SEQ ID NO 100; 66pp; English.

XX
 CC The present invention provides a Vitaxin antibody and a LM609 grafted antibody exhibiting selective binding affinity to alpha_v-beta_3. The invention is useful for treating alpha_v-beta_3-mediated diseases such as angiogenesis and restenosis. The present sequence is murine LM609
 CC antibody variable region CDR mutant peptide.
 XX
 SQ Sequence 10 AA;

```
Query Match      44.8%; Score 30; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. Nc. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy          2 YGSFFS 7
Db          5 YGSPYS 10
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Search completed: April 27, 2005, 15:49:16
Job time : 169 secs

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OM protein - protein search, using sw model

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(without alignments)

21.849 Million cell updates/sec

Title: US-10-088-681-2

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	34	50.7	8	4 US-08-467-344A-252	Sequence 252, APP
4	34	50.7	8	4 US-08-124-550B-252	Sequence 252, APP
5	30	44.8	6	1 US-08-424-957-6	Sequence 6, APP1
6	30	44.8	6	3 US-09-035-686-6	Sequence 6, APP1
7	30	44.8	10	4 US-09-339-922A-100	Sequence 100, APP
8	30	44.8	10	4 US-09-016-061-100	Sequence 100, APP
9	30	44.8	11	1 US-08-424-957-42	Sequence 42, APP1
10	30	44.8	11	3 US-09-335-686-42	Sequence 42, APP1
11	29	43.3	7	4 US-09-535-680B-10	Sequence 10, APP1
12	29	43.3	10	4 US-09-520-091-28	Sequence 28, APP1
13	28	41.8	11	3 US-09-186-938-6	Sequence 6, APP1
14	28	41.8	11	3 US-09-669-271A-6	Sequence 6, APP1
15	28	41.8	11	4 US-09-381-276-6	Sequence 6, APP1
16	27.5	41.0	9	1 US-08-931-645-50	Sequence 50, APP1
17	27.5	41.0	9	3 US-08-931-645-50	Sequence 50, APP1
18	27.5	41.0	9	5 PCT-US94-01258-50	Sequence 50, APP1
19	27.5	41.0	9	5 PCT-US95-11235-50	Sequence 50, APP1
20	27	40.3	6	1 US-08-277-660A-2	Sequence 2, APP1
21	27	40.3	6	1 US-08-424-957-2	Sequence 2, APP1
22	27	40.3	6	3 US-09-335-686-2	Sequence 2, APP1
23	27	40.3	6	4 US-09-081-975-1	Sequence 1, APP1
24	27	40.3	6	4 US-09-128-022B-130	Sequence 130, APP1
25	27	40.3	6	4 US-09-332-384-4	Sequence 4, APP1
26	27	40.3	7	1 US-08-277-660A-27	Sequence 27, APP1
27	27	40.3	7	1 US-08-424-957-15	Sequence 15, APP1

ALIGNMENTS

RESULT 1
US-08-469-260A-252
; Sequence 252, Application US/08469260A
; Patent No. 6451578

GENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATTAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHRHOPP
APPLICANT: JAMES C. ERGER
APPLICANT: SHERI L. BULJKAR
APPLICANT: ISA K. MUSHKAR
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469_260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424_550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6165
TELEFAX: 708-938-2623
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-469-260A-252
 Query Match 50.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELWTS 12
 Db 1 FSHLWTS 7

RESULT 2
 US-08-488-446-252
 ; Sequence 252, Application US/08467344A
 ; Patent No. 6536568
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; TAMI J. PILOT-MATIAS
 ; GEORGE J. DAWSON
 ; GEORGE G. SCHLAUDER
 ; SURESH M. DESAI
 ; THOMAS P. LEARY
 ; ANTHONY SCOTT MUERHOFF
 ; JAMES C. ERKER
 ; SHERI L. BUIJK
 ; ISA K. MUSHAHWAR
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 ; NUMBER OF SEQUENCES: 716
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 ; STREET: 100 ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,344A
 ; FILING DATE: 07-Jun-1995
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/424,550
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: POREMBSKI, PRISCILLA E.
 ; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-6365
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 252:
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/424,550
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: POREMBSKI, PRISCILLA E.
 ; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-6365
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 252:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-488-446-252

Query Match 50.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELWTS 12
 Db 1 FSHLWTS 7

US-08-467-344A-252
 ; Sequence 252, Application US/08467344A
 ; Patent No. 6536568
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; TAMI J. PILOT-MATIAS
 ; GEORGE J. DAWSON
 ; GEORGE G. SCHLAUDER
 ; SURESH M. DESAI
 ; THOMAS P. LEARY
 ; ANTHONY SCOTT MUERHOFF
 ; JAMES C. ERKER
 ; SHERI L. BUIJK
 ; ISA K. MUSHAHWAR
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 ; NUMBER OF SEQUENCES: 716
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 ; STREET: 100 ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/467,344A
 ; FILING DATE: 07-Jun-1995
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/424,550
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: POREMBSKI, PRISCILLA E.
 ; REGISTRATION NUMBER: 33,207
 ; REFERENCE/DOCKET NUMBER: 5527.PC.01
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 708-937-6365
 ; TELEFAX: 708-938-2623
 ; INFORMATION FOR SEQ ID NO: 252:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 8 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 252:
 ; US-08-467-344A-252

Query Match 50.7%; Score 34; DB 4; Length 8;
 Best Local Similarity 85.7%; Pred. No. 4.1e+05;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSELWTS 12
 Db 1 FSHLWTS 7

RESULT 4
 US-08-424-550B-252
 ; Sequence 252, Application US/08424550B
 ; Patent No. 6720166
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; TAMI J. PILOT-MATIAS
 ; GEORGE J. DAWSON
 ; GEORGE G. SCHLAUDER
 ; SURESH M. DESAI
 ; THOMAS P. LEARY
 ; ANTHONY SCOTT MUERHOFF
 ; ;

APPLICANT: JAMES C. ERKER
 APPLICANT: SHERI L. BUIJK
 APPLICANT: ISA K. MUSHAWAR
 TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 NUMBER OF SEQUENCES: 716
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 STREET: 100 ABBOTT PARK ROAD
 CITY: ABBOTT PARK
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550B
 FILING DATE: 4/35435
 ATTORNEY/AGENT INFORMATION:
 NAME: FOREMSKI, PRISCILLA B.
 REGISTRATION NUMBER: 33,207
 REFERENCE DOCKET NUMBER: 5527.PC.01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 708-937-6365
 TELEFAX: 708-938-2623
 INFORMATION FOR SEQ ID NO: 252:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-424-550B-252

Query Match Score 34; DB 4; Length 8;
 Best Local Similarity 85.%; Pred. No. 4.1e+05; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Miematches 1; Indels 0; Gaps 0;

RESULT 5
 US-08-424-957-6
 / Sequence 6, Application US/08424957
 / Patent No. 5770377
 / GENERAL INFORMATION:
 APPLICANT: Lane, David P.
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4117

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,550B
 FILING DATE: 4/35435
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4117

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,957
 FILING DATE: 19-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4117

APPLICATION NUMBER: US 08/277,660
 FILING DATE: 20-JUL-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 REFERENCE/DOCKET NUMBER: A-61228/WHD
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 US-08-424-957-6

Query Match Score 30; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05; Indels 0; Miematches 0; Gaps 0;

Qy 6 FSBLWTS 10
 Db 2 FSBLWTS 6

RESULT 6
 US-09-035-686-6
 / Sequence 6, Application US/09035686
 / Patent No. 6153391
 / GENERAL INFORMATION:
 APPLICANT: Picklesley, Steven M.
 ATTORNEY/AGENT INFORMATION:
 NAME: Lane, David P.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fiehr, Rohbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035,686
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/035,686
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4187

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,957
 FILING DATE: 19-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4117

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/424,957
 FILING DATE: 19-APR-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Dreyer, Walter H.
 REGISTRATION NUMBER: 24,190
 CORRESPONDENCE ADDRESS:
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: California
 COUNTRY: United States
 ZIP: 94111-4117

TOPOLOGY: unknown
 US-09-035-686-6

Query Match 44.8%; Score 30; DB 3; Length 6;
 Best Local Similarity 100.0%; Pred. No. 4.1e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSELM 10
 Db 2 FSELM 6

RESULT 7
 US-09-339-922A-100
 ; Sequence 100, Application US/09339922A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; PATENT NO.: 6531580
 ; TITLE OF INVENTION: Anti-Alphav Beta3 Recombinant Human Antibodies, Nucleic
 ; TITLE OF INVENTION: Acids Encoding Same and Methods of Use
 ; FILE REFERENCE: P-IX 3536
 ; CURRENT APPLICATION NUMBER: US/09/339,922A
 ; NUMBER OF SEQ ID NOS: 112
 ; SEQ ID NO: 100
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Mutated
 ; OTHER INFORMATION: complementarity determining region (CDR)
 ; US-09-339-922A-100

Query Match 44.8%; Score 30; DB 4; Length 10;
 Best Local Similarity 83.3%; Pred. No. 66;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
 Db 5 YGSFYS 10

RESULT 8
 US-09-16-061-100
 ; Sequence 100, Application US/09016061
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; APPLICANT: Glaser, Scott M.
 ; TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
 ; TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 92122
 ; TELEPHONE: (415) 781-1989
 ; FAX: (415) 398-3249
 ; TELEFAX: 910 277299
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/16,061
 ; FILING DATE: 30-JAN-1998
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/791,391
 ; FILING DATE: 30-JAN-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.

Query Match 44.8%; Score 30; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 72;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSELM 10
 Db 5 YGSFYS 10

RESULT 9
 US-08-424-957-42
 ; Sequence 42, Application US/08424957
 ; GENERAL INFORMATION:
 ; APPLICANT: Picklesley, Steven M.
 ; PATENT NO.: 5770377
 ; TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
 ; TITLE OF INVENTION: Protein and Therapeutic Application Thereof
 ; NUMBER OF SEQUENCES: 50
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Rohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 94111-4187
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/424,957
 ; FILING DATE: 19-APR-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/277,660
 ; FILING DATE: 20-JUL-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Dreger, Walter H.
 ; REGISTRATION NUMBER: 24,190
 ; REFERENCE/DOCKET NUMBER: A-61228/WHD
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 781-1989
 ; FAX: (415) 398-3249
 ; TELEFAX: 910 277299
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; US-08-424-957-42

Db 5 FSELMW 9

RESULT 10
US-09-035-686-42
Sequence 42, Application US/09035686
Patent No. 6153391
GENERAL INFORMATION:
APPLICANT: Pickleley, Steven M.
ATTORNEY: Lane, David P.
TITLE OF INVENTION: Interruption of Binding of MDM2 and P53
TITLE OF INVENTION: Protein and Therapeutic Application Thereof
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
ZIP: United States
94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/035, 686
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/424, 957
FILING DATE: 19-APR-1995
APPLICATION NUMBER: US 08/277, 660
FILING DATE: 20-JUL-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REFERENCE/DOCKET NUMBER: A-61228/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1919
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
STRANDEDNESS:
TOPOLOGY: unknown
US-09-035-686-42

Query Match Score 29; DB 4; Length 10;
Best Local Similarity 44.8%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 FSBLW 10
Db 5 FSELMW 9

RESULT 11
US-09-595-682B-10
Sequence 10, Application US/09595682B
Patent No. 6800483
GENERAL INFORMATION:
APPLICANT: Danks, Mary K.
APPLICANT: Potter, Phillip M.
APPLICANT: Houghcon, Peter J.
TITLE OF INVENTION: Compositions and Methods for Sensitizing and Inhibiting Growth of Tissue Cells
FILE REFERENCE: SU-005005
CURRENT APPLICATION NUMBER: US/09/595, 682B
CURRENT FILING DATE: 2000-01-16
PRIOR APPLICATION NUMBER: 60/075, 258

Query Match Score 29; DB 4; Length 10;
Best Local Similarity 43.3%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFSEBLW 10
Db 1 AFWTBLW 7

RESULT 12
US-09-620-091-28
Sequence 28, Application US/09620091
Patent No. 6716811
GENERAL INFORMATION:
APPLICANT: Chirila, Steven E.
APPLICANT: Balu, Palani
APPLICANT: Duffin, David J.
APPLICANT: Piplani, Sunil
APPLICANT: Merrill, Barbara McBown
APPLICANT: Schatz, Peter Joseph
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED SOFTWARE: PatentIn Ver. 2.1

Query Match Score 29; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SFSEBLW 10
Db 1 AFWTBLW 7

RESULT 13
US-09-186-958-6
Sequence 6, Application US/09186958B
Patent No. 6238860
GENERAL INFORMATION:
APPLICANT: Whelihan, E. Fayette
TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: Dyax-009, 0 US Sequence listing
CURRENT APPLICATION NUMBER: US/09/186, 958B
CURRENT FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1

Query Match Score 29; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 97;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 SFSEBLW 10
Db 3 SFWVBLW 9

FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
 US-09-186-958-6

Query Match 41.8%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 FFSEBLWTS 12
 Db 1 FFCALWPS 8

RESULT 14
 US-09-669-271A-6
 Sequence 6, Application US/09669271A
 Patent No. 6291197
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayette
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 FILE REFERENCE: Dyax 009.0 US Sequence Listing
 CURRENT APPLICATION NUMBER: US/09/669,271A
 CURRENT FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: 09/186,958
 PRIOR FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SEQ ID NO 6
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19
 US-09-669-271A-6

Query Match 41.8%; Score 28; DB 3; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 5 FFSEBLWTS 12
 Db 1 FFCALWPS 8

RESULT 15
 US-09-881-276-6
 Sequence 6, Application US/09881276
 Patent No. 6479641
 GENERAL INFORMATION:
 APPLICANT: Whelihan, E. Fayette
 TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
 FILE REFERENCE: DIX-009.0 US-2
 CURRENT APPLICATION NUMBER: US/09/881,276
 CURRENT FILING DATE: 2001-06-14
 PRIOR APPLICATION NUMBER: 09/169,271
 PRIOR FILING DATE: 2000-09-26
 PRIOR APPLICATION NUMBER: 09/186,958
 PRIOR FILING DATE: 1998-11-05
 NUMBER OF SEQ ID NOS: 27
 SOFTWARE: Microsoft Word 97
 SEQ ID NO 6
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide
 US-09-881-276-6

Query Match 41.8%; Score 28; DB 4; Length 11;
 Best Local Similarity 62.5%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GenCore version 5.1.6

OM protein - protein search, using SW mode!

Run on: April 27, 2005, 15:46:39 ; Search time 138 Seconds

(without alignments)
28.938 Million cell updates/secTitle: US-10-088-681-2
Perfect score: 67
Sequence: 1 EYGSPPSELWTS 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:
1: /cgns_6/prodata/2/pubpaas/us07_pubcomb.pep:*

2: /cgns_6/ptodata/2/pubpaas/fct_new_pub.pep:*

3: /cgns_6/ptodata/2/pubpaas/us06_pub.pep:*

4: /cgns_6/prodata/2/pubpaas/us06_pubcomb.pep:*

5: /cgns_6/ptodata/2/pubpaas/bctus_pubcomb.pep:*

6: /cgns_6/prodata/2/pubpaas/us07_new_pub.pep:*

7: /cgns_6/prodata/2/pubpaas/us08_new_pub.pep:*

8: /cgns_6/ptodata/2/pubpaas/us09_pubcomb.pep:*

9: /cgns_6/ptodata/2/pubpaas/us09a_pubcomb.pep:*

10: /cgns_6/prodata/2/pubpaas/us09b_pubcomb.pep:*

11: /cgns_6/peodata/2/pubpaas/us09c_pubcomb.pep:*

12: /cgns_6/prodata/2/pubpaas/us09_new_pub.pep:*

13: /cgns_6/prodata/2/pubpaas/us10a_pubcomb.pep:*

14: /cgns_6/peodata/2/pubpaas/us10b_pubcomb.pep:*

15: /cgns_6/prodata/2/pubpaas/us10c_pubcomb.pep:*

16: /cgns_6/prodata/2/pubpaas/us10d_pubcomb.pep:*

17: /cgns_6/peodata/2/pubpaas/us10_new_pub.pep:*

18: /cgns_6/prodata/2/pubpaas/us11_new_pub.pep:*

19: /cgns_6/prodata/2/pubpaas/us60_new_pub.pep:*

20: /cgns_6/peodata/2/pubpaas/us60_pubcomb.pep:*

Result No.	Score	Query Match	Length	DB ID	Description
1	34	50.7	6	16 US-10-221-042-2	Sequence 2, Appli
2	34	50.7	8	US-08-424-550B-252	Sequence 252, Appli
3	30	44.8	10	9 US-09-214-371-35	Sequence 35, Appli
4	30	44.8	10	9 US-09-214-371-36	Sequence 36, Appli
5	30	44.8	10	10 US-09-210-590-100	Sequence 100, Appli
6	30	44.8	10	14 US-10-905-231-100	Sequence 100, Appli
7	30	44.8	10	15 US-10-463-847-100	Sequence 100, Appli
8	29	43.3	10	17 US-10-659-207-28	Sequence 35, Appli
9	28	41.8	9	US-09-466-73A-35	Sequence 6, Appli
10	28	41.8	11	9 US-09-881-276-6	Sequence 56, Appli
11	28	41.8	11	15 US-10-417-895A-56	Sequence 83, Appli
12	27	40.3	6	9 US-09-214-371-83	Sequence 4, Appli
13	27	40.3	6	9 US-09-732-384-4	Sequence 3, Appli
14	27	40.3	6	13 US-10-155-059-1	Sequence 1, Appli
15	27	40.3	6	15 US-10-609-17-130	Sequence 130, Appli
16	27	40.3	6	15 US-10-632-388-130	Sequence 130, Appli
17	27	40.3	6	15 US-10-651-723-130	Sequence 130, Appli
18	27	40.3	6	15 US-10-645-761-130	Sequence 130, Appli
19	27	40.3	6	15 US-10-666-596-130	Sequence 130, Appli
20	27	40.3	6	15 US-10-653-948-130	Sequence 130, Appli
21	27	40.3	8	16 US-10-340-179-2	Sequence 2, Appli
22	27	40.3	8	16 US-10-340-179-3	Sequence 3, Appli
23	27	40.3	9	9 US-09-214-371-37	Sequence 17, Appli
24	27	40.3	9	9 US-09-214-371-38	Sequence 1, Appli
25	27	40.3	9	16 US-10-340-179-1	Sequence 107, Appli
26	27	40.3	10	17 US-10-726-332-107	Sequence 31, Appli
27	27	40.3	11	10 US-09-214-371-31	Sequence 17, Appli
28	27	40.3	12	9 US-09-214-371-17	Sequence 24, Appli
29	27	40.3	12	9 US-09-214-371-24	Sequence 25, Appli
30	27	40.3	12	9 US-09-214-371-25	Sequence 131, Appli
31	27	40.3	12	15 US-10-609-217-131	Sequence 132, Appli
32	27	40.3	12	15 US-10-609-217-132	Sequence 143, Appli
33	27	40.3	12	15 US-10-609-217-143	Sequence 144, Appli
34	27	40.3	12	15 US-10-609-217-144	Sequence 143, Appli
35	27	40.3	12	15 US-10-632-388-131	Sequence 131, Appli
36	27	40.3	12	15 US-10-632-388-132	Sequence 143, Appli
37	27	40.3	12	15 US-10-632-388-143	Sequence 144, Appli
38	27	40.3	12	15 US-10-632-388-144	Sequence 131, Appli
39	27	40.3	12	15 US-10-651-723-131	Sequence 132, Appli
40	27	40.3	12	15 US-10-651-723-132	Sequence 143, Appli
41	27	40.3	12	15 US-10-651-723-143	Sequence 144, Appli
42	27	40.3	12	15 US-10-651-723-144	Sequence 131, Appli
43	27	40.3	12	15 US-10-645-761-131	Sequence 132, Appli
44	27	40.3	12	15 US-10-645-761-132	Sequence 143, Appli
45	27	40.3	12	15 US-10-645-761-143	Sequence 143, Appli

ALIGNMENTS

RESULT 1	US-10-221-042-2	Sequence 2, Application US-10221042
		; Publication No. US2004012096A1
		; GENERAL INFORMATION:
		; APPLICANT: KANEKA CORPORATION
		; TITLE OF INVENTION: ADSORBENTS FOR DILATED CARDIOMYOPATHY
		; FILE REFERENCE: 12218/5
		; CURRENT APPLICATION NUMBER: US-10-221-042
		; CURRENT FILING DATE: 2002-10-09
		; PRIOR APPLICATION NUMBER: PCT/JP01/03026
		; PRIOR FILING DATE: 2001-04-09
		; PRIOR APPLICATION NUMBER: JP 2000-106915
		; PRIOR FILING DATE: 2000-04-07
		; NUMBER OF SEQ ID NOS: 13
		; SOFTWARE: Patentin version 3.1
		; SEQ ID NO: 2
		; LENGTH: 6
		; TYPE: PRT
		; ORGANISM: Artificial
		; FEATURE: peptide
		; OTHER INFORMATION: peptide
		; FEATURE:
		; NAME/KEY: MISC FEATURE
		; OTHER INFORMATION: Peptide having a binding affinity for an antibody against M2 muscarinic receptor
		; OTHER INFORMATION: beta-adrenoceptor and/or an antibody against M2 muscarinic receptor
		; OTHER INFORMATION: tor
		; US-10-221-042-2
Query Match	50.7%	Score 34; DB 16; Length 6;
Matches 6;	Conservative 0;	Mismatches 0; Indels 0;
Qy	1 EYGSEFF 6	
Db		1 EYGSEFF 6

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	50.7	6	16 US-10-221-042-2	Sequence 2, Appli
2	34	50.7	8	US-08-424-550B-252	Sequence 252, Appli
3	30	44.8	10	9 US-09-214-371-35	Sequence 35, Appli
4	30	44.8	10	9 US-09-214-371-36	Sequence 36, Appli
5	30	44.8	10	10 US-09-210-590-100	Sequence 100, Appli
6	30	44.8	10	14 US-10-905-231-100	Sequence 100, Appli
7	30	44.8	10	15 US-10-463-847-100	Sequence 100, Appli
8	29	43.3	10	17 US-10-659-207-28	Sequence 35, Appli
9	28	41.8	9	9 US-09-466-73A-35	Sequence 6, Appli
10	28	41.8	11	9 US-09-881-276-6	Sequence 56, Appli
11	28	41.8	11	15 US-10-417-895A-56	Sequence 83, Appli
12	27	40.3	6	9 US-09-214-371-83	Sequence 4, Appli
13	27	40.3	6	9 US-09-732-384-4	Sequence 3, Appli

RESULT 2 US-08-424-550B-252 Sequence 252, Application US/08424550B Publication No. US20020119447A1 GENERAL INFORMATION:

- APPLICANT: JOHN N. SIMONS
- APPLICANT: TAMI J. PILOT-MATIAS
- APPLICANT: GEORGE J. DAWSON
- APPLICANT: GEORGE G. SCHLAUDER
- APPLICANT: SURBESH M. DESAI
- APPLICANT: THOMAS P. LEARY
- APPLICANT: ANTHONY SCOTT NUERHOFF
- APPLICANT: JAMES C. ERKER
- APPLICANT: SHERI L. BUIJK
- APPLICANT: ISA K. MUSHAHWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE NUMBER OF SEQUENCES: 716

CORRESPONDENCE ADDRESS:

ADDRESSEE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD CITY: ABBOTT PARK STATE: IL COUNTRY: USA ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent In Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/424,550B FILING DATE: 435435 CLASSIFICATION: 435435 ATTORNEY/AGENT INFORMATION:

NAME: POREMBSKI, PRISCILLA B. REGISTRATION NUMBER: 33,207 REFERENCE DOCKET NUMBER: 5527.PC.01 TELECOMMUNICATION INFORMATION:

TELEPHONE: 708-938-6365 TELEFAX: 708-938-2623 INFORMATION FOR SEQ ID NO: 252: SEQUENCE CHARACTERISTICS:

SEQUENCE: 8 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-424-550B-252

Query Match Score 34; DB 8; Length 8; Best Local Similarity 85.7%; Pred. No. 1.3e+06; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FSBLWTS 12 ||||| 7 Db 1 FSHLWTS 7

TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2 FILE REFERENCE: 4-20937/A/PCT CURRENT APPLICATION NUMBER: US/09/214,371B PRIOR APPLICATION NUMBER: PCT/EP97/03549 NUMBER OF SEQ ID NOS: 83 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 35 LENGTH: 10 TYPE: PRT ORGANISM: Artificial Sequence FEATURES: OTHER INFORMATION: Description of Artificial Sequence:peptide NAME/KEY: VARIANT LOCATION: (1) OTHER INFORMATION: X = Ac-Cys (Acrd) NAME/KEY: VARIANT LOCATION: (10) OTHER INFORMATION: X = Pro-NH2 US-09-214-371-35

Query Match Score 30; DB 9; Length 10; Best Local Similarity 62.5%; Pred. No. 2.3e+02; Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GSFPSEIW 10 ||||| Db 2 GPTFSDLW 9

RESULT 4 US-09-214-371-36 Sequence 36, Application US/09214371B Patent No. US20010018511A1 GENERAL INFORMATION:

- APPLICANT: Lane, David
- APPLICANT: Bottger, Volker
- APPLICANT: Picklesley, Stephen
- APPLICANT: Chene, Patrick
- APPLICANT: Hochkeppel, Heinz-Kurt
- APPLICANT: Garcia-Echeverria, Carlos
- APPLICANT: Furet, Pascal

TITLE OF INVENTION: Inhibitors of the Interaction of P53 and MDM2 FILE REFERENCE: 4-20937/A/PCT CURRENT APPLICATION NUMBER: US/09/214,371B PRIOR APPLICATION NUMBER: PCT/EP97/03549 NUMBER OF SEQ ID NOS: 83 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 36 LENGTH: 10 TYPE: PRT ORGANISM: Artificial Sequence FEATURES: OTHER INFORMATION: Description of Artificial Sequence:peptide NAME/KEY: VARIANT LOCATION: (1) OTHER INFORMATION: X = Ac-Cys NAME/KEY: VARIANT LOCATION: (10) OTHER INFORMATION: X = Pro-NH2 US-09-214-371-36

Query Match Score 30; DB 9; Length 10; Best Local Similarity 62.5%; Pred. No. 2.3e+02; Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GSFPSEIW 10 ||||| Db 2 GPTFSDLW 9

RESULT 5

US-09-900-590-100
Sequence 1.00, Application US/09900590
Publication No. US20030028009A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
GLASER, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 1.00

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/09/900,590

FILING DATE: 06-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/016,061
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2965

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-3001
TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 100:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 100:
US-09-900-590-100

Query Match 44.8%; Score 30; DB 10; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
Db 5 YGSFYS 10

RESULT 6

US-10-305-231-100
Sequence 1.00, Application US/10305231
Publication No. US20030166872A1
GENERAL INFORMATION:
APPLICANT: Huse, William D.
WU, Herron

TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic Acids Encoding Same and Methods of Use

FILE REFERENCE: P-IX 5536
CURRENT APPLICATION NUMBER: US/10/305,231
CURRENT FILING DATE: 2002-11-25
PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/09/339,922
PRIOR FILING DATE: CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 100

Query Match 44.8%; Score 30; DB 15; Length 10;
Best Local Similarity 83.3%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YGSFFS 7
Db 5 YGSFYS 10

RESULT 8
US-10-659-207-28
Sequence 28; Application US/10659207
Publication No. US20050037959A1
GENERAL INFORMATION:
APPLICANT: CWIRLA, STEVEN E.
APPLICANT: BALU, PALANI
APPLICANT: DUFFIN, DAVID J.
APPLICANT: MERRILL, BARBARA MCEOWEN
APPLICANT: PIRIANT, SUNILIA
APPLICANT: SCHATZ, PETER JOSEPH
TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED TITLE OF INVENTION: USES FILE REFERENCE: 03/00-0014
CURRENT APPLICATION NUMBER: US/10/659,207
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: US/09/620,091
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 491
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-659-207-28

Query Match 43.3%; Score 29; DB 17; Length 10;
Best Local Similarity 71.4%; Pred. No. 3.e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 4 SPPSELW 10
| : |||
DB 3 SFNWELW 9

RESULT 9
US-09-486-734A-35
Sequence 35; Application US/09486734A
PATENT No. US20020164732A1
GENERAL INFORMATION:
APPLICANT: Chopin, Marie-Christine
APPLICANT: Chier, Florence
APPLICANT: Erlich, S. Dusko
APPLICANT: Gautier, Michel
APPLICANT: Schouler, Catherine
TITLE OF INVENTION: Resistance Mechanisms to Ic Type R/M
FILE REFERENCE: 33/339/196048
CURRENT APPLICATION NUMBER: US/09/486,734A
PRIOR APPLICATION NUMBER: PCT/FR98/01873
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 9

Query Match 41.8%; Score 28; DB 9; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.3e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
US-09-881-276-6
Sequence 6; Application US/09881276
PATENT No. US200203176A1
GENERAL INFORMATION:
APPLICANT: Wheilhan, E. Fayelle
TITLE OF INVENTION: Binding Moieties for Human Parvovirus B19
FILE REFERENCE: DXY-009.0 US-2
CURRENT APPLICATION NUMBER: US/09/881,276
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 09/669,271
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: 09/186,958
PRIOR FILING DATE: 1998-11-05
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Microsoft Word 97
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: parvovirus B19 binding polypeptide
US-09-881-276-6

Query Match 41.8%; Score 28; DB 9; Length 11;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5 PPSELMWS 12
| | | | |
DB 1 EFCALWPS 8

RESULT 11
US-10-417-895A-56
Sequence 56; Application US/10417895A
Publication No. US20040033369A1
GENERAL INFORMATION:
APPLICANT: Crea, Roberto
APPLICANT: Capuccilli, Guido
TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
FILE REFERENCE: 1551-2002-001
CURRENT APPLICATION NUMBER: US/10/417,895A
CURRENT FILING DATE: 2003-04-16
PRIOR APPLICATION NUMBER: 60/373,686
PRIOR FILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 86
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: variant peptide for third complementarity
OTHER INFORMATION: determining region of Fv region of an
OTHER INFORMATION: immunoglobulin
US-10-417-895A-56

Query Match 41.8%; Score 28; DB 15; Length 11;
Best Local Similarity 44.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 SPPSELWTS 12
| : |||:
DB 1 SYSSWSS 9

RESULT 12

US-09-214-371-83
 ; Sequence 83, Application US/09214371B
 ; Patent No. US2001008511A1
 GENERAL INFORMATION:
 ; APPLICANT: Lane, David
 ; APPLICANT: Bottger, Volker
 ; APPLICANT: Bottger, Angelica
 ; APPLICANT: Picklesley, Stephen
 ; APPLICANT: Chene, Patrick
 ; APPLICANT: Hochkeppel, Heinz-Kurt
 ; APPLICANT: Garcia-Echeverria, Carlos
 ; APPLICANT: Furet, Pascal
 TITLE OF INVENTION: Inhibitors of the Interaction of p53 and MDM2
 FILE REFERENCE: 4-20937/A/PCT
 CURRENT APPLICATION NUMBER: US/09/214-371B
 CURRENT FILING DATE: 1999-01-26
 PRIOR APPLICATION NUMBER: PCT/EP97/03549
 PRIOR FILING DATE: 1997-07-04
 NUMBER OF SEQ ID NOS: 83
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 83
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence;peptide, amin
 OTHER INFORMATION: Description of Artificial Sequence;peptide, amin
 OTHER INFORMATION: acid residues 18-23 of human p53
 US-09-214-371-83
 Query Match 40.3%; Score 27; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 6 FSBLW 10
 Db 2 FSDLW 6
 RESULT 13
 US-09-732-384-4
 Sequence 4, Application US/09732384
 Patent No. US20020132971A1
 GENERAL INFORMATION:
 ; APPLICANT: Yuan, Zhi-Min
 ; APPLICANT: Gu, Jijie
 TITLE OF INVENTION: Inhibition of p53 Degradation
 FILE REFERENCE: 21508-044
 CURRENT APPLICATION NUMBER: US/09/732,384
 CURRENT FILING DATE: 2000-12-07
 PRIOR APPLICATION NUMBER: 60/169,816
 PRIOR FILING DATE: 1999-12-08
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 4
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: Description of Artificial Sequence;Protein
 OTHER INFORMATION: Fragment not in inhibitory p53 polypeptide
 US-09-732-384-4
 Query Match 40.3%; Score 27; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;

RESULT 14
 US-10-155-059-1
 Sequence 14, Application US/10155059
 Publication No. US200214717A1
 GENERAL INFORMATION:
 ; APPLICANT: Kaelin, William
 ; Jost, Christine
 TITLE OF INVENTION: METHODS OF TREATMENT USING NBS-1, ANTIBODIES AND PROTEINS THERETO, AND USES OF THE ANTIBODIES
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESS: Nixon Peabody LLP
 STREET: 101 Federal Street
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows
 SOFTWARE: FastSEQ for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/155,059
 FILING DATE: 24-May-2002
 CLASSIFICATION: <Unknown>
 PRIORITY DATA:
 APPLICATION NUMBER: US/09/081,975
 FILING DATE: 12-MAY-1998
 APPLICATION NUMBER: 60/146,207
 FILING DATE: 12-MAY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Eisenstein, Ronald I
 REGISTRATION NUMBER: 30,628
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-345-6054
 TELEX: 617-345-1300
 TELEFAX: 617-345-6054
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-10-155-059-1
 Query Match 40.3%; Score 27; DB 13; Length 6;
 Best Local Similarity 80.0%; Pred. No. 1.3e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0;
 Gaps 0;
 Qy 6 FSBLW 10
 Db 2 FSDLW 6
 RESULT 15
 US-10-609-217-130
 Sequence 15, Application US/10609217
 Publication No. US20040044168A1
 GENERAL INFORMATION:
 ; APPLICANT: Feige, Ulrich
 ; APPLICANT: Liu, Chuan-fa
 ; APPLICANT: Cheetham, Janet C.
 ; APPLICANT: Boone, Thomas Charles
 TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
 FILE REFERENCE: A-527
 CURRENT APPLICATION NUMBER: US/10/609,217
 CURRENT FILING DATE: 2003-06-27
 PRIOR APPLICATION NUMBER: US/09/428,082B
 PRIOR FILING DATE: 1999-10-22
 PRIOR APPLICATION NUMBER: 60/105,371
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; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 130
; LENGTH: 6
; TYPE: PRT
; FEATURE:
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: MDM/HDM ANTAGONIST PEPTIDE
; US-10-609-217-130

Query Match 40.3%; Score 27; DB 15; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.3e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 6 FSELW 10
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Db 2 PSDLW 6

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